

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:05:16 ; Search time 36 Seconds

(without alignments)  
655.149 Million cell updates/sec

Title: US-10-000-157-6

Sequence: 1 MREPRLEGDSLSLFLQY.....ERRLYRVSLACVCPRVWG 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	985	100.0	177 22 AA004952	Human Interleukin PRO10272 polypepti
2	985	100.0	177 22 AAB47299	Human Interleukin PRO10272 polypepti
3	985	100.0	177 22 AAB87603	Human Interleukin PRO10272 polypepti
4	985	100.0	177 22 AAB07598	Human Interleukin PRO10272 polypepti
5	898	91.2	161 21 AAB07692	Human Interleukin PRO10272 polypepti
6	898	91.2	161 21 AAE18120	Human Interleukin PRO10272 polypepti
7	898	91.2	161 21 AAM52691	Human Interleukin PRO10272 polypepti
8	898	91.2	161 21 AAM47464	Human Interleukin PRO10272 polypepti
9	834	84.7	350 22 AAG29372	Novel human diagno
10	697	70.8	169 21 AAB07600	A murine Interleuk

11	697	70.8	169 21 AAB07694	A murine Interleuk
12	697	70.8	169 23 AAE18121	Mouse Interleukin-
13	697	70.8	169 23 AAM52692	Murine Interleukin
14	670	68.0	160 23 AAE18122	Mouse non-secreted
15	351.5	35.7	144 21 AAB07599	A murine Interleuk
16	351.5	35.7	144 21 AAB07693	A murine Interleuk
17	170.5	17.3	206 21 AAY44185	Human Interleukin
18	165.5	16.8	187 21 AAE23794	Mouse Interleukin
19	165.5	16.8	197 21 AAB18911	A novel polypeptid
20	165.5	16.8	197 21 AAB07602	A human Interleuki
21	165.5	16.8	197 21 AAB07684	A human Interleuki
22	165.5	16.8	197 21 AAY92238	Human Interleukin-
23	165.5	16.8	197 21 AAY44460	Human Interleukin
24	165.5	16.8	197 21 AAY53892	Amino acid sequenc
25	165.5	16.8	197 22 AAG66121	Human Interleukin
26	165.5	16.8	197 22 AA029247	Human PRO polypept
27	165.5	16.8	197 22 AA004951	Human Interleukin
28	165.5	16.8	197 23 AAE23792	Human LP-48 protei
29	165.5	16.8	227 22 AAE08676	Human Interleukin
30	165.5	16.8	227 22 AAE08679	Human Interleukin
31	165.5	16.8	227 22 AAE08680	Human Interleukin
32	165.5	16.8	227 22 AAE08681	Human Interleukin
33	165.5	16.8	227 22 AAE08682	Human Interleukin
34	165.5	16.8	227 22 AAE08683	Human Interleukin
35	165.5	16.8	227 22 AAE08684	Human Interleukin
36	165.5	16.8	425 21 AAY44462	Human Interleukin
37	165	16.8	223 22 AAE08685	Human mature Inter
38	163.5	16.6	227 22 AAE08686	Human Interleukin
39	161.5	16.4	227 22 AAE08687	Human Interleukin
40	160.5	16.3	227 22 AAE08688	Human Interleukin
41	157.5	16.0	227 22 AAE08689	Human Interleukin
42	156.5	15.9	227 22 AAE08688	Human Interleukin
43	156.5	15.9	227 22 AAE08689	Human Interleukin
44	156.5	15.9	227 22 AAE08691	Human Interleukin
45	156.5	15.9	227 22 AAE08693	Human Interleukin

## ALIGNMENTS

RESULT 1	AA004952	standard; Protein: 177 AA.
XX	AA004952:	
AC	24-OCT-2001 (first entry)	
XX		
DT	Human Interleukin 17E ligand, IL-17E.	
XX		
DE	Human Interleukin-17E ligand; IL-17E; agonist; antagonist; PRO10272; DNA 147531-2821; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; diabetes mellitus;	
KW	allergic disease; asthma; demyelinating disease;	
KW	degenerative cartilaginous disorder; transplantation associated disease.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Reptide	1..32
FT	Protein	/label= Signal-peptide
FT	Region	33..177
FT	Region	/label= Mature_IL_17E
FT	Region	44..50
FT	Modified-site	/note= "N-myristoylation site"
FT	Region	127..135
FT	Region	/note= "Tyrosine kinase phosphorylation site"
FT	Region	136..140
FT	Region	/note= "Asn is glycosylated"
FT	Region	150g..156
FT	Region	/note= "N-myristoylation site"
XX		
PN	WO200146420-A2.	

XX 28-JUN-2001.  
 XX 20-DEC-2000; 2000MO-US34956.  
 XX 23-DEC-1999; 99US-0172096.  
 XX 30-DEC-1999; 99MO-US31274.  
 XX 11-JAN-2000; 2000US-0175481.  
 XX 18-FEB-2000; 2000MO-US04341.  
 XX 02-MAR-2000; 2000MO-US05841.  
 XX 21-MAR-2000; 2000US-0191007.  
 XX 21-MAR-2000; 2000MO-US07532.  
 XX 02-JUN-2000; 2000MO-US35264.  
 XX 22-JUN-2000; 2000US-0213087.  
 XX 22-AUG-2000; 2000US-0644848.  
 XX 24-AUG-2000; 2000MO-US23328.  
 XX 24-OCT-2000; 2000US-0242837.  
 XX 10-NOV-2000; 2000MO-US30873.  
 XX 28-NOV-2000; 2000US-0253646.  
 XX 01-DEC-2000; 2000MO-US32678.  
 XX (GETH ) GENENTECH INC.  
 XX PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RJ;  
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;  
 XX MPI; 2001-451708/48.  
 XX DR N-PSDB; AAS09511.  
 XX PT Novel PRO polypeptides homologous to Interleukin-17, useful for the  
 XX PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 XX PT arthritis and diabetes.  
 XX Claim 10; Fig 6; 188pp; English.  
 XX The sequence is PRO10272 which is the human Interleukin 17E ligand,  
 XX IL-17E, encoded by DNA 147531-2821. A composition  
 XX CC containing ant/agonists to the PRO polypeptides or individual components  
 XX CC are useful for treating a mammal with an immune related disease, e.g.  
 XX CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
 XX CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 XX CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 XX CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 XX CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 XX CC disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 XX CC hypersensitivity, asthma, a transplantation associated disease, or a  
 XX CC chronic inflammatory demyelinating polyneuropathy. Treating a PRO1031 or  
 XX CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 XX CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 XX CC examples of the diseases and disorders are given in the specification.  
 XX SQ Sequence 177 AA;  
 XX  
 XX Query Match 100.0%; Score 985; DB 22; Length 177;  
 XX Best Local Similarity 100.0%; Pred. No. 2, 6e-93;  
 XX Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 MRRPRRLGSDSLISFLQVVAFLAMVGTHTYSHWPSCCPSKQDTSSEELRMSTVFP 60  
 XX DB 1 MRRPRRLGSDSLISFLQVVAFLAMVGTHTYSHWPSCCPSKQDTSSEELRMSTVFP 60  
 XX QY 61 PLPPARPNRHRESCRASEDPPLNSRAISPMRYELDRDLNRLPOLYHARCLCPHCVSLOT 120  
 XX DB 61 PLPPARPNRHRESCRASEDPPLNSRAISPMRYELDRDLNRLPOLYHARCLCPHCVSLOT 120  
 XX QY 121 GSHMDRGNSNELLHYNQTVFYRRPCHGEKGTHKGYCLERLRYSLACVCPRYPMG 177  
 XX DB 121 GSHMDRGNSNELLHYNQTVFYRRPCHGEKGTHKGYCLERLRYSLACVCPRYPMG 177  
 XX RESULT 2

AAB47299  
 ID AAB47299 standard; Protein: 177 AA.  
 XX AC AAB47299;  
 XX 22-AUG-2001 (first entry)  
 XX DE PRO10272 polypeptide.  
 XX PRO; PRO1081; PRO1274; PRO10272; proliferation; T-lymphocyte;  
 XX PRO1199; PRO1556; PRO1401; PRO10268; inhibition; stimulation;  
 XX infiltration; mononuclear cell; eosinophili; erythema multiforme;  
 XX polymorphonuclear neutrophil; PMN; antibody; immune-related disorder;  
 XX systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;  
 XX juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;  
 XX idiopathic inflammatory myopathy; Sjogren's syndrome; skin disease;  
 XX systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia; asthma;  
 XX autoimmune thrombocytopaenia; thyroiditis; diabetes mellitus; allergy;  
 XX immune-mediated renal disease; demyelination; central nervous system;  
 XX peripheral nervous system; idiopathic demyelinating polyneuropathy;  
 XX Guillain-Barre syndrome; hepatobiliary disease; eosinophilic pneumonia;  
 XX chronic active hepatitis; primary biliary cirrhosis; allergic rhinitis;  
 XX granulomatous hepatitis; sclerosing cholangitis; food hypersensitivity;  
 XX inflammatory bowel disease; gluten-sensitive enteropathy; urticaria;  
 XX Whipple's disease; idiopathic pulmonary fibrosis; contact dermatitis;  
 XX psoriasis; atopic dermatitis; hypersensitivity pneumonitis;  
 XX graft rejection; graft-versus-host disease.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT Peptide 1..32  
 XX FT /label= Signal peptide  
 XX FT Protein 33..177  
 XX FT /label= Mature PRO10272  
 XX FT Modified-site 44..50  
 XX FT /label= N-myristoylation site  
 XX FT Modified-site 127..135  
 XX FT /label= Tyrosine kinase phosphorylation site  
 XX FT Modified-site 136..140  
 XX FT /label= N-glycosylation site  
 XX FT Modified-site 150..156  
 XX FT /label= N-myristoylation site  
 XX PN WO200140465-A2.  
 XX 07-JUN-2001.  
 XX 10-NOV-2000; 2000MO-US30873.  
 XX PF 30-NOV-1999; 99MO-US28313.  
 XX PR 09-DEC-1999; 99US-0170262.  
 XX PR 23-DEC-1999; 99US-0172059.  
 XX PR 11-JAN-2000; 2000US-0175481.  
 XX PR 20-JAN-2000; 2000US-0177118.  
 XX PR 18-FEB-2000; 2000MO-US04342.  
 XX PR 03-MAR-2000; 2000US-0187202.  
 XX PR 30-MAY-2000; 2000MO-US14941.  
 XX PR 05-JUN-2000; 2000US-0209832.  
 XX PR 24-AUG-2000; 2000MO-US23328.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Fong S, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;  
 XX PI Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX DR MPI; 2001-381384/40.  
 XX DR N-PSDB; AAC85969.  
 XX PT Isolated PRO polypeptide useful for treat or diagnose an immune-related  
 XX PT disorder e.g. arthritis, asthma, allergy, diabetes or psoriasis.  
 XX PS Claim 1; Fig 18; 124pp; English.

XX The sequences given in AAB47291-99 show PRO polypeptides. PRO1081, CC PRO1274 and PRO1072 stimulate the proliferation of T-lymphocytes and CC PRO1599, PRO1556, PRO4401 and PRO10268 inhibit the proliferation of CC T-lymphocytes. PRO1754 and PRO9912 act to enhance the infiltration of CC mononuclear cells, eosinophils or polymorphonuclear neutrophils (PMN) CC into the tissue of a mammal. The PRO cDNA's and antibodies which CC bind to them, are used to treat an immune-related disorder in a CC mammal. Such disorders include systemic lupus erythematosus, CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a CC spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, CC diabetes mellitus, immune-mediated renal disease, a demyelinating CC disease of the central or peripheral nervous system, idiopathic CC demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic CC inflammatory demyelinating polyneuropathy, a hepatobiliary disease, CC infectious or autoimmune chronic active hepatitis, primary biliary CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's CC disease, an autoimmune or immune-mediated skin disease, a bulious skin CC disease, erythema multiforme, contact dermatitis, psoriasis, an CC allergic disease, asthma, allergic rhinitis, atopic dermatitis, food CC hypersensitivity, urticaria, an immunologic disease of the lung, CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity CC pneumonitis, a transplantation associated disease, graft rejection or CC graft-versus-host disease.

SO Sequence 177 AA:

Query Match 100.0%; Score 985; DB 22; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2.6e-93;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCSPKSGDTSSELRKSTVPVP 60  
DB 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCSPKSGDTSSELRKSTVPVP 60  
QY 61 PLEPARPNRHPSRCASDGPLNSRAISPMRYELDRDLNRLPDLTHARCLCPHCVSLOT 120  
DB 61 PLEPARPNRHPSRCASDGPLNSRAISPMRYELDRDLNRLPDLTHARCLCPHCVSLOT 120  
QY 121 GSHMDPRGNSSELYHNQTVFYRRPCHGKGTGKGYCLERRLRVSLACVCPRPVWG 177  
DB 121 GSHMDPRGNSSELYHNQTVFYRRPCHGKGTGKGYCLERRLRVSLACVCPRPVWG 177

RESULT 3  
AAB87603 standard; Protein: 177 AA.

XX AAB87603;  
XX 15-MAY-2001 (first entry)  
XX Human PRO10272.  
XX Human; PRO protein; mapping.  
XX Homo sapiens.  
XX MO200116318-A2.  
XX 08-MAR-2001.  
XX 24-AUG-2000; 2000MO-US233328.  
XX 01-SEP-1999; 99MO-US20111.  
XX 15-SEP-1999; 99MO-US21090.  
XX 07-DEC-1999; 99US-0169495.  
XX 09-DEC-1999; 99US-0170262.  
XX 11-JAN-2000; 2000US-0175481.  
XX 18-FEB-2000; 2000MO-US04341.

PR 18-FEB-2000; 2000MO-US04342.  
PR 22-FEB-2000; 2000MO-US04414.  
PR 01-MAR-2000; 2000MO-US05601.  
PR 03-MAR-2000; 2000US-0187202.  
PR 25-APR-2000; 2000US-0199397.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 05-JUN-2000; 2000US-0209832.

XX (GETH ) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI,

XX WPI; 2001-183260/18.

DR N-PSDB; AAF92135.

XX Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
PT chromosome and gene mapping.

XX Claim 12; Fig 156; 278pp; English.

XX The present sequence is a human PRO polypeptide (secreted and  
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or  
CC anti-PRO antibodies are useful for preparation of a medicament useful in  
CC the treatment of a condition which is responsive to the PRO protein,  
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be  
CC employed as molecular weight markers for protein electrophoresis. The PRO  
CC coding sequence has applications in molecular biology, including use as  
CC hybridisation probes, and in chromosome and gene mapping.

SO Sequence 177 AA:

Query Match 100.0%; Score 985; DB 22; Length 177;  
Best Local Similarity 100.0%; Pred. No. 2.6e-93;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCSPKSGDTSSELRKSTVPVP 60  
DB 1 MRRRLGDSLSLFLQYVAFVFLAMVGTHTYSHWPCSPKSGDTSSELRKSTVPVP 60  
QY 61 PLEPARPNRHPSRCASDGPLNSRAISPMRYELDRDLNRLPDLTHARCLCPHCVSLOT 120  
DB 61 PLEPARPNRHPSRCASDGPLNSRAISPMRYELDRDLNRLPDLTHARCLCPHCVSLOT 120  
QY 121 GSHMDPRGNSSELYHNQTVFYRRPCHGKGTGKGYCLERRLRVSLACVCPRPVWG 177  
DB 121 GSHMDPRGNSSELYHNQTVFYRRPCHGKGTGKGYCLERRLRVSLACVCPRPVWG 177

RESULT 4  
AAB07598 standard; Protein: 161 AA.

XX AAB07598;  
XX 07-NOV-2000 (first entry)  
XX A human interleukin (IL) 174 polypeptide.  
XX Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
XX IL-177; IL-171; cell proliferation; cancer.  
XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..16

XX Modified-site /note- "signal peptide"

XX Modified-site /note- "calcium phosphorylation site"

XX Modified-site /note- "calcium phosphorylation site"

XX Modified-site 12..16

FT Protein /note- "myristoylation site"  
 FT 17..161  
 FT /note- "mature protein"  
 FT 21  
 FT /note- "phosphorylation site"  
 FT 21..24  
 FT /note- "CAMP protein kinase phosphorylation site"  
 FT 23  
 FT /note- "phosphorylation site"  
 FT 41..43  
 FT /note- "protein kinase C phosphorylation site"  
 FT 43  
 FT /note- "phosphorylation site"  
 FT 45..47  
 FT /note- "calcium phosphorylation site"  
 FT 53  
 FT /note- "phosphorylation site"  
 FT 53..56  
 FT /note- "CAMP protein kinase phosphorylation site"  
 FT 56  
 FT /note- "phosphorylation site"  
 FT 95  
 FT /note- "phosphorylation site"  
 FT 95..98  
 FT /note- "CAMP protein kinase phosphorylation site"  
 FT 95..102  
 FT /note- "tyrosine kinase site"  
 FT 98  
 FT /note- "phosphorylation site"  
 FT 104..107  
 FT /note- "N-glycosylation site"  
 FT 115..119  
 FT /note- "myristoylation site"  
 FT 118..122  
 FT /note- "myristoylation site"  
 FT 119..121  
 FT /note- "protein kinase C phosphorylation site"  
 FT 131  
 FT /note- "phosphorylation site"  
 PN W0200042188-A2.  
 XX 20-JUL-2000.  
 XX 10-JAN-2000; 2000MO-US00006.  
 XX 11-JAN-1999; 99US-0228822.  
 XX (SCHE ) SCHERING CORP.  
 XX Gorman DM, Bazan JF, Kastelein RA;  
 XX WPI: 2000-466130/40.  
 DR N-PSDB: AAB58986.  
 XX  
 PT New isolated polynucleotide encoding a mammalian Interleukin-17 like  
 XX protein used to identify genes for homologous proteins -  
 PS Claim 11; Page 16; 111pp; English.  
 XX  
 CC The present sequence represents an interleukin-174 (IL-174) polypeptide.  
 CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
 CC member of a new group of interleukins, IL-170 polypeptides. The members  
 CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
 CC protein can be used to treat abnormal proliferation e.g. cancer  
 CC or degenerative conditions. Antibodies can be used in diagnostic  
 CC methods to detect over production of IL-170 protein in cells or body  
 CC fluids.  
 XX  
 SQ Sequence 161 AA;  
 Query Match 91.2%; Score 898; DB 21; Length 161;  
 Best local Similarity 100.0%; Pred. No. 2.1e-84;

Matches	159; Conservative	0; Mismatches	0; Indels
QY 19	OYVAFIAMVWGTHHTYHWPSCCPKSGQDTSSELLRMSTVPPLEPARPRHRESCASE 78		
Db 3	OYVAFIAMVWGTHHTYHWPSCCPKSGQDTSSELLRMSTVPPLEPARPRHRESCASE 62		
QY 79	DGPLNSRAISPMRYELDRDLNRLPOLYHARCICPHCVSLQTSQSHMDPRNSSELLYHNOT 138		
Db 63	DGPLNSRAISPMRYELDRDLNRLPOLYHARCICPHCVSLQTSQSHMDPRNSSELLYHNOT 122		
QY 139	VFYRRPCHEKGTNKGVCLEERLYRVSLACVCVPRVWG 177		
Db 123	VFYRRPCHEKGTNKGVCLEERLYRVSLACVCVPRVWG 161		
RESULT 5			
AAB07692	AAB07692 standard; Protein; 161 AA.		
ID	AAB07692; (first entry)		
AC	AAB07692; (first entry)		
XX	A human Interleukin-174 polypeptide.		
DE	Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;		
XX	IL-174; IL-176; IL-177; cell proliferation; cancer.		
KM	Homo sapiens.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Homo sapiens.		
PH	Key		
FT	Peptide		
FT	1..16		
FT	/note- "signal peptide"		
FT	15..17		
FT	/note- "calcium phosphorylation site"		
FT	16..18		
FT	/note- "calcium phosphorylation site"		
FT	12..16		
FT	/note- "myristoylation site"		
FT	17..161		
FT	/note- "mature protein"		
FT	21		
FT	/note- "phosphorylation site"		
FT	21..24		
FT	/note- "CAMP protein kinase phosphorylation site"		
FT	23		
FT	/note- "phosphorylation site"		
FT	41..43		
FT	/note- "protein kinase C phosphorylation site"		
FT	43		
FT	/note- "phosphorylation site"		
FT	45..47		
FT	/note- "calcium phosphorylation site"		
FT	53		
FT	/note- "phosphorylation site"		
FT	53..56		
FT	/note- "CAMP protein kinase phosphorylation site"		
FT	56		
FT	/note- "phosphorylation site"		
FT	95		
FT	/note- "phosphorylation site"		
FT	95..98		
FT	/note- "CAMP protein kinase phosphorylation site"		
FT	95..102		
FT	/note- "tyrosine kinase site"		
FT	98		
FT	/note- "phosphorylation site"		
FT	104..107		
FT	/note- "N-glycosylation site"		
FT	115..119		
FT	/note- "myristoylation site"		
FT	118..122		
FT	/note- "myristoylation site"		



FT Modified-site 119..121  
 FT /note="protein kinase C phosphorylation site"  
 FT Modified-site 131  
 FT /note="phosphorylation site"  
 XX MO200042187-A1.  
 XX 20-JUL-2000.  
 XX 10-JAN-2000; 2000WO-US00005.  
 XX 11-JAN-1999; 99US-0229402.  
 XX (SCHE ) SCHERING CORP.  
 PA Gorman DM, Bazan JF, Kastelein RA;  
 PI WPI; 2000-476060/41.  
 DR N-PSDB; AAS59158.  
 XX  
 PS New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 PT Interleukin-171 (IL-171), useful for recombinant production of IL-171  
 PT physiology or development -  
 XX  
 XX Disclosure; Page 19; 11pp; English.  
 CC The present sequence represents an interleukin (IL)-174 polypeptide.  
 CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 CC referred to as IL-17). The specification also describes homologues  
 CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 CC cDNA molecules which code for related or homologous proteins. The  
 CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g., cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.  
 CC  
 XX Sequence 161 AA:  
 SQ  
 Query Match 91.2%; Score 898; DB 21; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-84;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPPLPARPNRHPESCRASE 78  
 DB 3 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPPLPARPNRHPESCRASE 62  
 QY 79 DGPLNSRAISPMRYELDRDLNRLPQDLVHARCLCPHCVSLQSGHMDPRGNSSELLYHNQT 138  
 DB 63 DGPLNSRAISPMRYELDRDLNRLPQDLVHARCLCPHCVSLQSGHMDPRGNSSELLYHNQT 122  
 QY 139 VFYRPPCHGKGTGKGYCLERLRYVSLACVCPVRRVWG 177  
 DB 123 VFYRPPCHGKGTGKGYCLERLRYVSLACVCPVRRVWG 161

KW Infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
 KW leukaemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 KW cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FH Peptide 1..16  
 FT /label= Signal\_peptide  
 FT Protein 17..161  
 FT /label= Mature\_IL-17L\_protein  
 XX  
 PN WO200208285-A2.  
 XX 31-JAN-2002.  
 XX  
 XX 21-JUN-2001; 2001WO-US19861.  
 PF 22-JUN-2000; 2000US-213125P.  
 PR 02-FEB-2001; 2001US-266159P.  
 PR 16-MAR-2001; 2001US-0810384.  
 XX  
 PA (AMGE-) AMGEN INC.  
 PI Medlock E, Yeh R, Silbiger SM, Elliott GS, Nguyen HQ, Jing S;  
 DR WPI; 2002-155217/20.  
 DR N-PSDB; AAD28771.  
 XX  
 PT Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
 PT polypeptides useful in the treatment, prevention and diagnosis of  
 PT diseases e.g. cancer -  
 XX  
 PS Claim 13; Fig 1; 242pp; English.  
 CC The invention relates to nucleic acid molecules encoding Interleukin 17  
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating  
 CC (pre)neurotic arthritis, osteoarthritis, inflammatory joint disease;  
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
 CC disease, transplant rejection, graft vs. host disease); Infections (HIV,  
 CC hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia,  
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 CC (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 CC (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy  
 CC atherosclerosis, heart failure, angiogenesis); tumour cancers (lymphoma  
 CC leukaemia); reproductive (infertility, miscarriage, endometriosis), eye  
 CC blindness, retinal neuropathy) and treatment of diseases involving  
 CC inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
 CC protein.  
 CC  
 XX Sequence 161 AA:  
 SQ  
 Query Match 91.2%; Score 898; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2,1e-84;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPPLPARPNRHPESCRASE 78  
 DB 3 QVAVFLAMVWGTHYSHMPSCCPSKGGDTSEELRMSTVPPPLPARPNRHPESCRASE 62  
 QY 79 DGPLNSRAISPMRYELDRDLNRLPQDLVHARCLCPHCVSLQSGHMDPRGNSSELLYHNQT 138  
 DB 63 DGPLNSRAISPMRYELDRDLNRLPQDLVHARCLCPHCVSLQSGHMDPRGNSSELLYHNQT 122  
 QY 139 VFYRPPCHGKGTGKGYCLERLRYVSLACVCPVRRVWG 177  
 DB 123 VFYRPPCHGKGTGKGYCLERLRYVSLACVCPVRRVWG 161

RESULT 7
AAM52691
ID AAM52691 standard; Protein; 161 AA.
XX AC
XX AAM52691;
XX DT
DE 26-FEB-2002 (first entry)
XX DE Human Interleukin 174 (IL-174).
XX XX
KW Human; interleukin 174; IL-174; cytokine; Th2 response;
KW Innate immune response; inflammation; gut cell growth;
KW extramedullary haematopoiesis; antibody response; granuloma formation;
KW autoimmune condition; multiple sclerosis; systemic lupus erythematosus;
KW rheumatoid arthritis; diabetes; psoriasis; infectious agent;
KW inflammatory condition; Crohn's disease; ulcerative colitis;
KW pancreatitis; hepatitis; allergy; Th2-mediated condition;
KW systemic anaphylactic response; skin hypersensitivity response;
KW dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator;
KW antinflammatory; antiarthritic; antidiabetic; antifungal;
KW dermatological; neuroprotective; antiallergic; agonist; antagonist.
XX OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT /label= Signal_peptide
FT Protein 17..161
ET /label= Mature_IL-174
PX PN MO200179288-A2.
PD PD 25-OCT-2001.
XX PF 17-APR-2001; 2001MO-US12493.
XX PR 18-APR-2000; 2000US-198488P.
XX PA (SCHE ) SCHERING CORP.
XX PI Hurst SD, Zurawski SM, Rennick DM;
XX DR WPI: 2002-034343/04.
DR N-PSTDB; ABA02393.
XX PT Administering an interleukin 174 agonist or antagonist to a mammal
PT regulates various immune and inflammatory responses and is useful to
PT treat for example autoimmune diseases, allergies or response to an
PT infection _
XX PS Examples; Page 27-28; 29pp; English.
XX XX
CC The invention relates to methods of directing an immune response in a
CC mammal by the administration of an agonist or antagonist of the cytokine
CC interleukin 174 (IL-174). Administration of an IL-174 agonist directs the
CC immune response towards a Th2 response, stimulates an innate immune
CC response, augments the inflammatory response from epithelial or
CC fibroblast cells, induces gut cell growth, promotes extramedullary
CC haematopoiesis, or augments an antibody response in serum and faecal
CC material, while administration of an IL-174 antagonist directs the immune
CC response away from a Th2 type response, and prevents inflammation or
CC granuloma formation. IL-174 agonists may be used to treat autoimmune
CC conditions (particularly multiple sclerosis, diabetes or psoriasis), a response
CC erythematous, rheumatoid arthritis, diabetes or psoriasis), a response
CC to an infectious agent, or inflammatory conditions such as Crohn's
CC disease, ulcerative colitis, pancreatitis, or hepatitis. IL-174
CC antagonists may be used to treat inflammatory, allergic or Th2-mediated
CC conditions (e.g., systemic anaphylactic response, skin hypersensitivity
CC response, dermatitis, asthma, fibrosis, or eosinophilic gastritis). The
CC present sequence represents human IL-174.
XX XX

Seq	Sequence	161 AA:	91.2%: Score 898; DB 23; length 161;
Query Match	Best Local Similarity	100.0%;	Pred. No. 2.1e-84;
Matches 159;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	QVAFVLAWMTHTYTHSHNPSCPSKGGDTSEELLMWSTVPVPLEPAPRNHRESCRASE	78	
Db	3 QVAFVLAWMTHTYTHSHNPSCPSKGGDTSEELLMWSTVPVPLEPAPRNHRESCRASE	62	
OY	79 DGPLNSRAISPMRYELBDNLNRPDLTYHARCLPHCVSLQTGSHMDPGNSSELLYHNOT	138	
Db	63 DGPLNSRAISPMRYELBDNLNRPDLTYHARCLPHCVSLQTGSHMDPGNSSELLYHNOT	122	
OY	139 VFRRPCHGEGKTHKGYCLERLYVSLACVCPVRPWG	177	
Db	123 VFRRPCHGEGKTHKGYCLERLYVSLACVCPVRPWG	161	
RESULT 8			
AA047464	AA047464		
AC	AA047464;		
DT	1-FEB-2002 (first entry)		
DE	Human IL-17 receptor like protein ligand, IL-17E.		
XX	Human: IL-17 receptor-like protein; immunomodulatory; antiarthritic; antiproliferative; antimicrobial; anorectic; neuroprotective; antihistaminic; antiallergic; dermatological; cytostatic; gene therapy; interleukin 17; immune system disorder; infection; weight; reproductive; neuronal dysfunction; lung; asthma; skin; eczema; kidney; inflammation; glomerulonephritis; bone; osteoporosis; vascular system; haemophilia; eye; tumour; IL-17E.		
XX			
OS	Homo. sapiens.		
PN	WD200168705-A2.		
PD	20-SEP-2001.		
PF	15-MAR-2001; 2001WO-US08688.		
PR	15-MAR-2000; 2000US-189923P.		
PR	12-MAY-2000; 2000US-204208P.		
PR	27-NOV-2000; 2000US-072323Z.		
PR	02-FEB-2001; 2001US-266159P.		
XX			
PA	(AMGE-) AMGEN INC.		
PI	Jing S, Medlock E, Yeh R, Silbiger SM, Elliot GS, Nguyen HQ;		
XX			
DR	WPI: 2002-055100/07.		
DR	N-PSDB: ABA03213.		
XX			
PT	Three human nucleic acids encoding interleukin 17 (IL-17) receptor like		
PT	polypeptides, useful for treating, diagnosing, ameliorating or		
PT	preventing immune system disorders (e.g. psoriatic arthritis) and		
PT	infections (e.g. viral infections)		
PS	Example 7, Page 234-235, 239pp; English.		
XX			
CC	The present invention relates to novel human nucleic acids encoding		
CC	interleukin 17 (IL-17) receptor like proteins (see ABA03200-ABA03202,		
CC	AA047456, AA047458 and AA047459). The IL-17 receptor like proteins and		
CC	coding sequences are useful for treating a pathological condition related		
CC	to immune system dysfunction (e.g. psoriatic arthritis), infections (e.g.		
CC	viral infections), weight disorders (e.g. obesity), neuronal dysfunction		
CC	disorders (e.g. Alzheimer's disease), lung disorders (e.g. asthma), skin		
CC	disorders (e.g. eczema), kidney disorders (e.g. glomerulonephritis),		
CC	bone disease (e.g. osteoporosis), vascular system disorders (e.g.		

CC Ischaemia), eye disorders, reproductive disorders, tumours and  
 CC inflammation. The present sequence is the protein sequence for IL-17E, a  
 CC human IL-17 receptor like protein ligand.  
 CC  
 SO Sequence 161 AA;

Query Match 91.2%; Score 898; DB 23; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-84;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 QVAFPLAMVGTHTYSHMPCSCPSKGDTSSELLRMSTVPVPLEPARPNRHPESCRASE 78  
 DB 3 QVAFPLAMVGTHTYSHMPCSCPSKGDTSSELLRMSTVPVPLEPARPNRHPESCRASE 62  
 QY 79 DGPLNSRAISPMRYELDRDLNRLPDOLYHARCICPHCVSLQSGSHMDPRGNSLLYHNOT 138  
 DB 63 DGPLNSRAISPMRYELDRDLNRLPDOLYHARCICPHCVSLQSGSHMDPRGNSLLYHNOT 122  
 QY 139 VFYRPPCHGEKGTGHKGYCLERRLYRVSLACVCPRPVWG 177  
 DB 123 VFYRPPCHGEKGTGHKGYCLERRLYRVSLACVCPRPVWG 161

RESULT 9  
 ABG29372  
 ID ABG29372 standard; Protein; 350 AA.  
 AC ABG29372;  
 DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #29363.  
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 OS Homo sapiens.

XX MO200175067-A2.  
 XX 11-OCT-2001.

XX 30-MAR-2001; 2001MO-US08631.

XX 31-MAR-2000; 2000US-0540217.  
 XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSO INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.  
 XX N-PSDB: AAS93559.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

PS Claim 20; SEQ ID No 59731; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WPIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
 CC  
 SO Sequence 350 AA;

Query Match 84.7%; Score 834; DB 22; Length 350;  
 Best Local Similarity 91.1%; Pred. No. 2.1e-77;  
 Matches 153; Conservative 1; Mismatches 4; Indels 10; Gaps 2;

QY 19 QVAFPLAMVGTHTYSHMPCSCPSKGDTSSELLRMSTVPVPLEPARPNRHPESCRASE 78  
 DB 28 RYVAFPLAMVGTHTYSHMPCSCPSKGDTSSELLRMSTVPVPLEPARPNRHPESCRASE 87  
 QY 79 DGPLNSRAISPMRYE-----LDRDLNRLPDOLYHARCICPHCVSLQSGSHMDPRGNS 130  
 DB 88 DGPLNSRAISPMRYEEDKCRPHRLDRDLNRLPDOLYHARCICPHCVSLQSGSHMDPRGNS 147  
 QY 131 ELLYHNOTVFYRPPCHGEKGTGHKGYCLERRLYRVSLAC--VCVPRPVW 176  
 DB 148 ELLYHNOTVFYRPPCHGEKGTGHKGYCLERRLYRVSLACGALVGPPIKM 195

RESULT 10  
 AAB07600  
 ID AAB07600 standard; Protein; 169 AA.  
 AC AAB07600;  
 DT 07-NOV-2000 (first entry)

DE A murine interleukin (IL) 174 polypeptide.  
 KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
 KW IL-177; IL-171; cell proliferation; cancer.

XX Mus sp.

XX Key Location/Qualifiers  
 XX FH 1..16  
 XX FH Peptide

FT Modified-site 2..4 "signal peptide"

FT Protein /note- "protein kinase C phosphorylation site"

FT Modified-site 17..169  
 FT /note- "mature protein"

FT Modified-site 18..20  
 FT /note- "calcium phosphorylation site"

FT Modified-site 29..32  
 FT /note- "cAMP protein kinase phosphorylation site"

FT Modified-site 29  
 FT /note- "phosphorylation site"

FT Modified-site 31  
 FT /note- "phosphorylation site"

FT Modified-site 49..51  
 FT /note- "phosphorylation site"

FT Modified-site 51  
 FT /note- "protein kinase C phosphorylation site"

FT Modified-site 53  
 FT /note- "phosphorylation site"

FT Modified-site 53..55  
 FT /note- "phosphorylation site"

FT Modified-site 61  
 FT /note- "calcium phosphorylation site"

FT Modified-site 61..64  
 FT /note- "phosphorylation site"

FT Modified-site 64  
 FT /note- "cAMP protein kinase phosphorylation site"

FT Modified-site  
 FT /note- "phosphorylation site"

FT	Modified-site	67..69	/note- "calcium phosphorylation site"
FT	Modified-site	112..114	/note- "N-glycosylation site"
FT	Modified-site	123..127	/note- "myristoylation site"
FT	Modified-site	127..129	/note- "protein kinase C phosphorylation site"
FT	Modified-site	139	/note- "phosphorylation site"
FT	Modified-site	141	/note- "phosphorylation site"
FT	Modified-site	141	/note- "phosphorylation site"
PN	W0200042188-A2.		
XX	20-JUL-2000.		
XX	10-JAN-2000; 2000MO-U500006.		
XX	11-JAN-1999; 99US-0228822.		
XX	(SCHE ) SCHERING CORP.		
XX	Gorman DM, Bazan JF, Kastelein RA;		
XX	WPI; 2000-466130/40.		
XX	N-PSDB; AAA58988.		
XX	New isolated polynucleotide encoding a mammalian interleukin-17 like		
XX	protein used to identify genes for homologous proteins -		
XX	Claim 11; Page 18; 11pp; English.		
XX	The present sequence represents an interleukin-174 (IL-174) polypeptide.		
XX	The polypeptide is an IL-17-like (CtLA-8 related) protein. It is a		
XX	member of a new group of interleukins, IL-170 polypeptides. The members		
XX	comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170		
XX	protein can be used to treat abnormal proliferation e.g. cancer		
XX	or degenerative conditions. Antibodies can be used in diagnostic		
XX	methods to detect over production of IL-170 protein in cells or body		
XX	fluids.		
XX	Sequence 169 AA:		
XX	Query Match	70.8%;	Score 697; DB 21; Length 169;
XX	Best Local Similarity	76.5%;	Pred. No. 1.1e-63;
XX	Matches 127; Conservative	9;	Mismatches 22; Indels 8; Gaps 1;
QY	19 QVAFLAMVGTHTY-----SHMPSCPSKQDTSELLRMSTVYPVPLEPARPNH 70		
DB	3 QAVAFIAMVGTHTVSLRIQEGCSHLPPSCPSKQEPPEEMLKMSASVSPPEPLSHTHH 62		
QY	71 PESCRASEDGPLNSRAISPMRYELDLNLTLPDLYHARCLPGVSLQSGSHMDPRGNS 130		
DB	63 AESCRASKDGPLNSRAISPMRYELDLNLTLPDLYHARCLPGVSLQSGSHMDPLGNS 122		
QY	131 ELLVHNOTVYRRCGEGKTHKGYCLERLYEVSILACYCVAPRPVYM 176		
DB	123 VPLVHNOTVYRRCGEGKTHKGYCLERLYEVSILACYCVAPRPVYM 168		
XX	RESULT 11		
XX	AAB07694		
XX	AAB07694 standard; Protein: 169 AA.		
XX	AAB07694:		
XX	07-NOV-2000 (first entry)		
XX	A murine interleukin-174 polypeptide.		
XX	Interleukin; IL-173; cytokine; CtLA-8; IL-17; IL-175; IL-172; IL-173;		
XX	IL-174; IL-176; IL-177; cell proliferation; cancer.		

XX	OS	Mus sp.	
XX	FH	Key	Location/Qualifiers
FT	FT	Peptide	1..16
FT	FT	Modified-site	/note= "signal peptide"
FT	FT	Protein	2..4
FT	FT	Modified-site	/note= "protein kinase C phosphorylation site"
FT	FT	Modified-site	17..169
FT	FT	Modified-site	/note= "mature protein"
FT	FT	Modified-site	18..20
FT	FT	Modified-site	/note= "calcium phosphorylation site"
FT	FT	Modified-site	29..32
FT	FT	Modified-site	/note= "CaM protein kinase phosphorylation site"
FT	FT	Modified-site	29
FT	FT	Modified-site	/note= "phosphorylation site"
FT	FT	Modified-site	31
FT	FT	Modified-site	/note= "phosphorylation site"
FT	FT	Modified-site	49..51
FT	FT	Modified-site	/note= "protein kinase C phosphorylation site"
FT	FT	Modified-site	51
FT	FT	Modified-site	/note= "phosphorylation site"
FT	FT	Modified-site	53
FT	FT	Modified-site	/note= "phosphorylation site"
FT	FT	Modified-site	53..55
FT	FT	Modified-site	/note= "calcium phosphorylation site"
FT	FT	Modified-site	61
FT	FT	Modified-site	/note= "phosphorylation site"
FT	FT	Modified-site	61..64
FT	FT	Modified-site	/note= "CaM protein kinase phosphorylation site"
FT	FT	Modified-site	64
FT	FT	Modified-site	/note= "phosphorylation site"
FT	FT	Modified-site	67..69
FT	FT	Modified-site	/note= "calcium phosphorylation site"
FT	FT	Modified-site	112..114
FT	FT	Modified-site	/note= "N-glycosylation site"
FT	FT	Modified-site	123..127
FT	FT	Modified-site	/note= "myristoylation site"
FT	FT	Modified-site	127..129
FT	FT	Modified-site	/note= "protein kinase C phosphorylation site"
FT	FT	Modified-site	139
FT	FT	Modified-site	/note= "phosphorylation site"
FT	FT	Modified-site	141
FT	FT	Modified-site	/note= "phosphorylation site"
XX	PX	NO200042187-A1.	
XX	PN	20-JUL-2000.	
XX	PD	10-JAN-2000; 2000WO-US00005.	
XX	PP	11-JAN-1999; 98US-0229402.	
XX	PR	(SCHE ) SCHERING CORP.	
PA	PA	Gorman DM, Bazan JF, Kastelein RA;	
PI	PI	MP1: 2000-476060/41.	
PS	PS	N-PESDB: AAN59160.	
PT	PT	New DNA sequence encoding a mammalian homolog of CTLA-8, designated	
PT	PT	interleukin-171 (IL-171), useful for recombinant production of IL-171	
PT	PT	which can be used for treating conditions associated with abnormal	
PT	PT	physiology or development -	
XX	XX	Disclosure; Page 21; 11pp; English.	
CC	CC	The present sequence represents an interleukin (IL)-17A polypeptide.	
CC	CC	It is a mammalian homologue of the cytokine designated CTLA-8 (also	
CC	CC	referred to as IL-17). The specification also describes homologues	
CC	CC	IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA	
CC	CC	sequence encoding IL-171 is useful for identifying genes, mRNA and	
CC	CC	cDNA molecules which code for related or homologous proteins. The	

IL-17 protein, antibodies against IL-17, and compounds which have binding affinity to IL-17 are useful in treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions, or degenerative conditions. The IL-17 protein can be used in kits and assay methods for identifying compounds that selectively bind to IL-17.

Sequence 169 AA:

Query Match 70.8%; Score 697; DB 21; Length 169;  
Best Local Similarity 76.5%; Pred. No. 1,1e-63;  
Matches 127; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

OY 19 QVAFVFLAMVMTHTY-----SHWPCSCPSCGQDTSEELLRWSTVPPLEPARPNR 70  
DB 3 QAVAFVFLAMVGTHTVSLRIQEGCSHLPCSCPEKEQPEPEMLKWSASVSPPEPLSHTH 62  
OY 71 PESCRASEDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSCHMDPRGNS 130  
DB 63 AESCRASKDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSCHMDPRGNS 122  
OY 131 ELLYHNOVTFYRRPCHGEGKTHKGYCLERLYRVSLACVCPRRVM 176  
DB 123 VPLVHNOVTFYRRPCHGEGKTHKGYCLERLYRVSLACVCPRRVM 168

RESULT 12  
AAE18121  
ID AAE18121 standard; Protein; 169 AA.

AAE18121;

07-MAY-2002 (first entry)

Mouse Interleukin-17 like (IL-17L) protein.

Mouse: Interleukin-17 like; IL-17L; immune system dysfunction; diabetes; cytostatic; multiple sclerosis; rheumatoid arthritis; therapy; lupus; inflammatory bowel disease; neuronal dysfunction; transplant rejection; autoimmune disorder; lung; skin; kidney; bone; eye; vascular system; infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis; cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema; eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease; epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis; leukemia; retinal neuropathy; infertility; miscarriage; inflammation; cancer.

Mus musculus.

Key Location/Qualifiers

Peptide 1..18 /label= Signal\_peptide

Protein 19..169 /label= Mature\_IL\_17L\_protein

MO200208285-A2.

31-JAN-2002.

21-JUN-2001; 2001WO-US19861.

22-JUN-2000; 2000US-211325P.

02-FEB-2001; 2001US-266159P.

16-MAR-2001; 2001US-0810384.

(AMGE-) AMGEN INC.

Medlock E, Yeh R, Silbiger SM, Elliott GS, Nguyen HQ, Jing S;  
WPI; 2002-155217/20.  
N-PSDB; AAD28772.

Nucleic acid molecules encoding Interleukin 17 (IL-17) - like

polypeptides useful in the treatment, prevention and diagnosis of diseases e.g. cancer -  
Claim 13; Fig 2; 242pp; English.

The invention relates to nucleic acid molecules encoding Interleukin 17 (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels of IL-17 protein in an animal. The IL-17 protein is useful for treating, preventing or ameliorating a disease, such as immune system dysfunction (rheumatoid arthritis, osteoarthritis, inflammatory joint disease); autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel disease, transplant rejection, graft vs. host disease); infections (HIV, hepatitis, bacterial); weight disorders (obesity, anorexia, cachexia, sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung (acute respiratory distress syndrome, cystic fibrosis, emphysema); skin (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone (osteoporosis, Paget's disease, hypercalcaemia) vascular system (epilepsy atherosclerosis, heart failure, angiodysplasia); tumours, cancers (lymphoma leukemia); reproductive (infertility, miscarriage, endometriosis); eye (blindness, retinal neuropathy) and treatment of diseases involving inflammation. The present sequence is mouse Interleukin-17 like (IL-17L) protein.

Query Match 70.8%; Score 697; DB 23; Length 169;  
Best Local Similarity 76.5%; Pred. No. 1,1e-63;  
Matches 127; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

OY 19 QVAFVFLAMVMTHTY-----SHWPCSCPSCGQDTSEELLRWSTVPPLEPARPNR 70  
DB 3 QAVAFVFLAMVGTHTVSLRIQEGCSHLPCSCPEKEQPEPEMLKWSASVSPPEPLSHTH 62  
OY 71 PESCRASEDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSCHMDPRGNS 130  
DB 63 AESCRASKDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSCHMDPRGNS 122  
OY 131 ELLYHNOVTFYRRPCHGEGKTHKGYCLERLYRVSLACVCPRRVM 176  
DB 123 VPLVHNOVTFYRRPCHGEGKTHKGYCLERLYRVSLACVCPRRVM 168

RESULT 13  
AAM52692  
ID AAM52692 standard; Protein; 169 AA.

AAM52692;

26-FEB-2002 (first entry)

Murine Interleukin 174 (IL-174).

Mouse; murine; Interleukin 174; IL-174; cytokine; Th2 response; innate immune response; inflammation; gut cell growth; extramedullary haematopoiesis; antibody response; granuloma formation; autoimmune condition; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; diabetes; psoriasis; infectious agent; inflammatory condition; Crohn's disease; ulcerative colitis; pancreaticitis; hepatitis; allergy; Th2-mediated condition; systemic anaphylactic response; skin hypersensitivity response; dermatitis; asthma; fibrosis; eosinophilic gastritis; immunomodulator; antiinflammatory; antiarthritic; antidiabetic; antifungal; dermatological; neuroprotective; antiallergic; agonist; antagonist.

Mus sp.

Key Location/Qualifiers

Peptide 1..16 /label= Signal\_peptide

Protein 17..169 /label= Mature\_IL-174

MO200179288-A2.



ID AAB07599 standard; Protein: 144 AA.  
 XX AAB07599;  
 AC  
 XX 07-NOV-2000 (first entry)  
 DT  
 XX A murine Interleukin (IL) 174 polypeptide.  
 DE  
 XX Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
 KM IL-177; IL-171; cell proliferation; cancer.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200042188-A2.  
 XX  
 PD 20-JUL-2000.  
 XX  
 PF 10-JAN-2000; 2000WO-US00006.  
 XX  
 PR 11-JAN-1999; 99US-0228822.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Gorman DM, Bazan JF, Kastelein RA;  
 XX  
 DR WPI: 2000-466130/40.  
 DR N-PSDB; AAB58987.  
 XX  
 PT New isolated polynucleotide encoding a mammalian Interleukin-17 like  
 PT protein used to identify genes for homologous proteins -  
 XX  
 PS Claim 11; Page 17; 111pp; English.  
 XX  
 CC The present sequence represents an Interleukin-174 (IL-174) polypeptide.  
 CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a  
 CC member of a new group of interleukins, IL-170 polypeptides. The members  
 CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
 CC protein can be used to treat abnormal proliferation e.g. cancer  
 CC or degenerative conditions. Antibodies can be used in diagnostic  
 CC methods to detect over production of IL-170 protein in cells or body  
 CC fluids.  
 CC  
 SQ Sequence 144 AA;  
 QY Query Match 35.7%; Score 351.5; DB 21; Length 144;  
 Best Local Similarity 59.8%; Pred. No. 3.1e-28;  
 Matches 70; Conservative 6; Mismatches 36; Indels 5; Gaps 2;  
 QY 59 VPP--LEPARPNRHPESCRASEDGPLNSRAISPMRYELDRDLNRLPODLYHARCLCPHCY 116  
 DB 19 IPRASEPHEPRR---ILQCGQGPPLNSRAISPMRYELDRDLNRLPODLYHARCLCPHCY 75  
 QY 117 SLOGTGSHMDPRGNSSELYHNQTVFYRRPCHGEKTHKGYCLERRLYRVSILACVCVRP 173  
 DB 76 TLQGTGSHMDPLGNVSPPLYNQTVFYRRPCHMARVPIAATAWSAGLPSTLGLCYCAAP 132

Search completed: February 26, 2003, 09:31:37  
 Job time : 37 secs





05 FT Modified-site 119..121  
 04 FT /note="protein kinase C phosphorylation site"  
 03 FT Modified-site 131  
 02 FT /note="phosphorylation site"  
 01 FT MO200042187-A1.  
 00 PD 20-JUL-2000.  
 00 PD 10-JAN-2000; 2000WO-US00005.  
 00 PD 11-JAN-1999; 990US-0229402.  
 00 PD (SCHE ) SCHERING CORP.  
 00 PD Gorman DM, Bazan JF, Kastelein RA;  
 00 PD WPI: 2000-476060/41.  
 00 PD N-PSDB; AAA59158.  
 00 PD  
 00 PD New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 00 PD Interleukin-171 (IL-171), useful for recombinant production of IL-171  
 00 PD which can be used for treating conditions associated with abnormal  
 00 PD physiology or development.  
 00 PD  
 00 PD Disclosure: Page 19; 11pp; English.  
 00 PD  
 00 PD The present sequence represents an interleukin (IL)-174 polypeptide.  
 00 PD It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 00 PD referred to as IL-17). The specification also describes homologues  
 00 PD IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 00 PD sequence encoding IL-171 is useful for identifying genes, mRNA and  
 00 PD cDNA molecules which code for related or homologous proteins. The  
 00 PD IL-171 protein, antibodies against IL-171, and compounds which have  
 00 PD binding affinity to IL-171 are useful in treatment of conditions  
 00 PD associated with abnormal physiology or development, including abnormal  
 00 PD proliferation, e.g. cancerous conditions, or degenerative conditions.  
 00 PD The IL-171 protein can be used in kits and assay methods for identifying  
 00 PD compounds that selectively bind to IL-171.  
 00 PD  
 00 PD Sequence 161 AA;  
 00 PD  
 00 PD Query Match  
 00 PD Best Local Similarity 91.2%; Score 898; DB 21; Length 161;  
 00 PD Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 00 PD  
 00 PD 19 QVAFLLAMVGTHTYSHMPCSCPKGDTSEELRMSTVPPVPLEPAPNRHPECRASE 78  
 00 PD 3 QVAFLLAMVGTHTYSHMPCSCPKGDTSEELRMSTVPPVPLEPAPNRHPECRASE 78  
 00 PD 79 DGPLNSRAISPMRYEELDRDLNRLPQDLVYHARCICPHCVSLQTSQSHMPRGNSSELLYNQ 138  
 00 PD 63 DGPLNSRAISPMRYEELDRDLNRLPQDLVYHARCICPHCVSLQTSQSHMPRGNSSELLYNQ 138  
 00 PD 139 VFYRRPCHGEKGTGKGYCCLERRLRYSLACVCPRPVWG 177  
 00 PD 123 VFYRRPCHGEKGTGKGYCCLERRLRYSLACVCPRPVWG 161  
 00 PD  
 00 PD RESULT 6  
 00 PD ID AAE18120  
 00 PD AC AAE18120;  
 00 PD  
 00 PD 17-MAY-2002 (first entry)  
 00 PD  
 00 PD Interleukin-17 like (IL-17L) protein.  
 00 PD  
 00 PD Interleukin-17 like; IL-17L; immune system dysfunction; diabetes;  
 00 PD rheumatoid arthritis; therapy; lupus;  
 00 PD disease; neuronal dysfunction; transplacental rejection;  
 00 PD eye; skin; kidney; bone; eye; vascular system;

KW Infection; hepatitis; obesity; anorexia; cachexia; glomerulonephritis;  
 KW cystic fibrosis; Alzheimer's disease; Parkinson's disease; emphysema;  
 KW eczema; sepsis; psoriasis; wound healing; osteoporosis; Paget's disease;  
 KW epilepsy; atherosclerosis; heart failure; angiogenesis; endometriosis;  
 KW leukemia; retinal neuropathy; infertility; miscarriage; inflammation;  
 KW cancer.  
 OS Homo sapiens.  
 FH Key  
 FT Peptide 1..16  
 FT /label= signal\_peptide  
 FT Protein 17..161  
 FT /label= Mature\_IL-17L\_protein  
 PN WO200208285-A2.  
 PD 31-JAN-2002.  
 PD 21-JUN-2001; 2001WO-US19861.  
 PD 22-JUN-2000; 2000US-213125P.  
 PD 02-FEB-2001; 2001US-266159P.  
 PD 16-MAR-2001; 2001US-0810384.  
 PD (AMGE-) AMGEN INC.  
 PD Medlock E, Yeh R, Slibiger SM, Elliott GS, Nguyen HQ, Jing S;  
 PD WPI: 2002-155217/20.  
 PD N-PSDB; AAD28771.  
 DR  
 DR Nucleic acid molecules encoding Interleukin 17 (IL-17) - like  
 PT polypeptides useful in the treatment, prevention and diagnosis of  
 PT diseases e.g. cancer  
 PS Claim 13; Fig 1; 242pp; English.  
 CC  
 CC The invention relates to nucleic acid molecules encoding Interleukin 17  
 CC (IL-17)-like polypeptides. IL-17 DNA can be used to modulate the levels  
 CC of IL-17 protein in an animal. The IL-17 protein is useful for treating,  
 CC preventing or ameliorating a disease, such as immune system dysfunction,  
 CC rheumatoid arthritis, osteoarthritis, inflammatory joint disease;  
 CC autoimmune (multiple sclerosis, lupus, diabetes, inflammatory bowel  
 CC disease, transplant rejection, graft vs. host disease); infections (HIV,  
 CC hepatitis, bacterial), weight disorders (obesity, anorexia, cachexia,  
 CC sepsis); neuronal dysfunction (Alzheimer's, Parkinson's disease); lung  
 CC (asthma), respiratory distress syndrome, cystic fibrosis, emphysema); skin  
 CC (psoriasis, eczema, wound healing); kidney (glomerulonephritis); bone  
 CC (osteoporosis, Paget's disease, hypercalcaemia); vascular system (epilepsy  
 CC atherosclerosis, heart failure, angiogenesis); tumors, cancers (lymphoma  
 CC leukemia); reproductive (infertility, miscarriage, endometriosis), eye  
 CC (blindness, retinal neuropathy) and treatment of diseases involving  
 CC inflammation. The present sequence is human Interleukin-17 like (IL-17L)  
 CC protein.  
 CC  
 CC Sequence 161 AA;  
 CC  
 CC Query Match  
 CC Best Local Similarity 91.2%; Score 898; DB 23; Length 161;  
 CC Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 19 QVAFLLAMVGTHTYSHMPCSCPKGDTSEELRMSTVPPVPLEPAPNRHPECRASE 78  
 CC 3 QVAFLLAMVGTHTYSHMPCSCPKGDTSEELRMSTVPPVPLEPAPNRHPECRASE 78  
 CC 79 DGPLNSRAISPMRYEELDRDLNRLPQDLVYHARCICPHCVSLQTSQSHMPRGNSSELLYNQ 138  
 CC 63 DGPLNSRAISPMRYEELDRDLNRLPQDLVYHARCICPHCVSLQTSQSHMPRGNSSELLYNQ 138  
 CC 139 VFYRRPCHGEKGTGKGYCCLERRLRYSLACVCPRPVWG 177  
 CC 123 VFYRRPCHGEKGTGKGYCCLERRLRYSLACVCPRPVWG 161  
 CC  
 CC Db

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:31:41 ; Search time 14 Seconds  
(without alignments)  
371.990 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985  
Sequence: 1 MRRPRRGEDESSLSLFLQV.....ERRLYVSLACVCPRYWG 177

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued Patents AA:\*  
2: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	12.4	153	1	US-08-514-014-12 Sequence 12, Appl
2	122	12.4	153	2	US-08-833-823-12 Sequence 12, Appl
3	122	12.4	163	3	US-09-034-810-2 Sequence 2, Appl
4	122	12.4	163	3	US-08-685-239-2 Sequence 2, Appl
5	121	12.3	205	4	US-09-724-864-37 Sequence 37, Appl
6	105.5	10.7	155	4	US-08-432-994A-8 Sequence 8, Appl
7	93.5	9.5	151	2	US-08-620-694A-8 Sequence 8, Appl
8	93.5	9.5	151	3	US-09-034-810-6 Sequence 8, Appl
9	93.5	9.5	151	3	US-09-022-255-8 Sequence 8, Appl
10	93.5	9.5	151	3	US-09-022-255-8 Sequence 8, Appl
11	93.5	9.5	151	3	US-08-685-239-6 Sequence 8, Appl
12	93.5	9.5	151	3	US-09-022-253-8 Sequence 8, Appl
13	93.5	9.5	151	3	US-09-022-253-8 Sequence 8, Appl
14	93.5	9.5	151	4	US-09-022-259-8 Sequence 8, Appl
15	93.5	9.5	151	4	US-09-022-257-8 Sequence 8, Appl
16	93.5	9.5	151	4	US-08-432-994A-4 Sequence 4, Appl
17	91	9.2	150	3	US-09-034-810-4 Sequence 4, Appl
18	91	9.2	150	3	US-08-685-239-4 Sequence 4, Appl
19	91	9.2	150	4	US-08-432-994A-2 Sequence 4, Appl
20	91	9.2	158	4	US-08-432-994A-10 Sequence 10, Appl
21	86	8.7	158	2	US-08-620-694A-7 Sequence 7, Appl
22	86	8.7	158	3	US-09-022-255-7 Sequence 7, Appl
23	86	8.7	158	3	US-09-022-255-7 Sequence 7, Appl
24	86	8.7	158	3	US-09-022-253-7 Sequence 7, Appl
25	86	8.7	158	3	US-09-022-253-7 Sequence 7, Appl
26	86	8.7	158	3	US-09-022-253-7 Sequence 7, Appl
27	86	8.7	158	4	US-09-022-257-7 Sequence 7, Appl

28	77.5	7.9	961	5	PCR-US93-11225-4	Sequence 4, Appl
29	76.5	7.7	1323	1	US-08-026-138E-4	Sequence 4, Appl
30	75.5	7.8	1185	4	US-08-664-962B-2	Sequence 2, Appl
31	75.5	7.7	1185	4	US-09-311-743-2	Sequence 2, Appl
32	75	7.6	514	4	US-08-974-549A-605	Sequence 605, App
33	74.5	7.6	807	4	US-08-974-549A-5	Sequence 5, App
34	74.5	7.6	1132	3	US-08-851-843A-225	Sequence 225, App
35	74.5	7.6	1132	4	US-08-974-549A-2	Sequence 225, App
36	74.5	7.6	1132	4	US-08-974-549A-344	Sequence 344, App
37	74.5	7.6	1132	4	US-08-854-050-225	Sequence 225, App
38	74.5	7.6	1132	4	US-09-430-323-225	Sequence 225, App
39	74.5	7.6	1132	4	US-09-128-354-2	Sequence 225, App
40	74.5	7.6	1132	4	US-09-675-321-2	Sequence 2, Appl
41	74.5	7.6	1132	4	US-08-974-549A-611	Sequence 2, Appl
42	74.5	7.6	1132	4	US-08-974-549A-611	Sequence 2, Appl
43	74.5	7.6	1189	4	US-08-974-549A-613	Sequence 611, App
44	74.5	7.6	1200	4	US-08-974-549A-613	Sequence 613, App
45	74.5	7.6	1285	4	US-08-974-549A-600	Sequence 600, App

## ALIGNMENTS

RESULT 1  
US-08-514-014-12

Sequence 12, Application US/08514014  
Patent No. 5707829

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKeough

TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/514,014

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G16000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 153 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-514-014-12

Query Match

Best Local Similarity 26.2%, Pred. No. 6.6e-06;

Matches 45; Conservative 25; Mismatches 60; Indels 42; Gaps 8;

12 SLISL-FLQVAVFLAMVGTHTSYWPCSCPSKODTSELLRWSTVVP-----PLEPAR 66

8 SILGLAFLEAFAARKIRPVGHFTFOKPEPCSC-----PVPGSGMKLDIGI 51



APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKenough  
APPLICANT: Goldman, Samuel  
APPLICANT: Piltman, Debora  
APPLICANT: M, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, Joann  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,239  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 163 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-239-2

Query Match 12.4%; Score 122; DB 3; Length 163;  
Best Local Similarity 26.2%; Pred. No. 7.2e-06;  
Matches 45; Conservative 25; Mismatches 60; Indels 42; Gaps 8;

QY 12 SLTSL-FLQVAFILAMVGTHTSHMPCSCPSKQDTSEELLRSTYVVP-----PLEPAR 66  
DB 18 SLGLAFLEAARKIKPKGHTFFQKPESCP-----PVPGSMKLDIGI 61  
QY 67 PRRHPECSRASEDGPLNRAISPMRYELDRNLRLPDOLYHARCPCPHCVSLQTSMDP 126  
DB 62 IN---ENGVSMRNEISTSPWNTVTMDPRRPSSEVQAQCRNIGCTINAO----- 111  
QY 127 RENSELLYN-----QTVFYRRPCHGEKGTHTKGYCLERRLYRLACVCP 173  
DB 112 -GKEDISNVSPIQOETLVVRRK---HGGCSVSFOLEKVL--VTVGCTCTP 157

RESULT 5  
US-09-724-864-37  
Sequence 37, Application US/09724864  
Patent No. 6380362  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Murison, James G.  
TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
FILE REFERENCE: 11000.105001  
CURRENT APPLICATION NUMBER: US/09/724,864  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 37  
LENGTH: 205  
TYPE: PRT  
ORGANISM: Mouse  
US-09-724-864-37

Query Match 12.3%; Score 121; DB 4; Length 205;  
Best Local Similarity 27.1%; Pred. No. 1.2e-05;  
Matches 42; Conservative 19; Mismatches 58; Indels 36; Gaps 7;

QY 41 PSKQDPTSEELLR-----WSTVPPELEPARPRHPECSRASE---DGPLN 83  
DB 35 PROCDAREELLEDQYGLAGVLSAFHHTLQIGREQARNASCAGGAADRRPRPTN 94  
QY 84 SRAISPMRYELDRNLRLPDOLYHARCPCPHCVSLQTSMDPENSELLYNQVVF--- 140  
DB 95 LRSVPMAYRSTYDPAFRPLRYLPAYCLCRCL--TGLY-----GEDEFRRSTVFSPA 147  
QY 141 --YRR--PCHGKGTHTKGYCLERRLYRLACVCP 171  
DB 148 VVLRRTAACAGAGRSVYAEHY-----TIPVGTCTV 177

RESULT 6  
US-08-432-994A-8  
Sequence 8, Application US/08432994A  
Patent No. 6274711  
GENERAL INFORMATION:  
APPLICANT: Goistein, Pierre  
APPLICANT: Rouvier, Eric  
APPLICANT: Fossiez, Francois  
APPLICANT: Lebecque, Serge J.E.  
APPLICANT: Djossou, Odile  
APPLICANT: Banchereau, Jacques  
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,994A  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/250,846  
FILING DATE: 27-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/177,747  
FILING DATE: 05-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077,203  
FILING DATE: 14-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX038K3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 155 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-432-994A-8

Query Match 10.7%; Score 105.5; DB 4; Length 151;  
Best Local Similarity 27.1%; Pred. No. 0.00044;  
Matches 45; Conservative 27; Mismatches 73; Indels 21; Gaps 8;

QY 11 SLSLSFLQVAVFLAMVWGHTHTYSHMPCSCPSKQDSTSELLRMSTVPVP-PLFAPRPNR 69  
6 TSLVLLLL--LSLDAIYKAGITIPRNPCPSSEKKNFPR-----TVMNLTINHRNTVT 58  
DB 70 HPECSRASEDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSMDPRGN 129  
59 NPK--RSD--YNNRSTSPWTLHRNDDORPSYIWEAK--CRLLGCIINAGNDYHMN 111  
QY 130 SELLYHNOGVFYRRPC---HGEKGTNKGCTLERRLYRSLACVCPVPRV 175  
112 SVPIQDELIVLRREPPH---CPNSFRLKIL--VVGCTCVTPIV 151  
DB

RESULT 7  
US-08-620-694A-8  
Sequence 8, Application US/08620694A  
Patent No. 5869286

GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanle  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286el Receptor That Blinds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-08-620-694A-8

Query Match 9.5%; Score 93.5; DB 2; Length 151;  
Best Local Similarity 23.0%; Pred. No. 0.009;  
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

QY 11 SLSLSFLQVAVFLAMVWGHTHTYSHMPCSCPSKQDSTSELL-----RMSTVPVPLEPA 65  
6 TSLVLLLL--LSIDCIYKSEITSAQTPRCILANNSFPRSVVYVTLISIRNMNT----- 54  
DB 66 RPNRHPESCRASEDGPLNSRAISPMRYELDRDLNRLPDLYHARCICPHCVSLQTSMD 125  
55 -----SKRASD--YNNRSTSPWTLHRNDDORPSYIWEAKCRILGCVNAD----- 99  
QY 126 PRGNSELYHNOGVFYRRPC---HGEKGTNKGCTLERRLYRSLACVCPVPRV 175  
100 --GNVD--YIMNSVPIQDELIVLRKGGQPCPNRFLKML--VVGCTCVTPIV 147  
DB

RESULT 8  
US-09-034-810-6  
Sequence 6, Application US/09034810  
Patent No. 6043344

GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Ml, Sha  
APPLICANT: Neden, Steven  
APPLICANT: Giannotti, John  
APPLICANT: Golden/Fleet, Margaret  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,810  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,239  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-034-810-6

Query Match 9.5%; Score 93.5; DB 3; Length 151;  
Best Local Similarity 23.0%; Pred. No. 0.009;

QY 11 SSSLSLQVAVAFAMVAGTHTTYSHPSCCCSKQDOSTEELL-----RWSVVPVPLEPA 65  
 Db 6 TSVLLLEL- - -SIDCIYKSEITSAQTQPCILANNSPFRSVAVTLISIRNMT----- 54  
 QY 66 RPNRHPESCRASEGDEPLNSRAISPMWRLELDLDLRLQDLYHACLCPHCYSLDQTGSHMD 125  
 Db 55 -----SKRKSD---YNNRSTSPWTLHRNEDDQRYTSVLEACRYLGCYNAD----- 99  
 QY 126 PRGSEILLYNNQTVFYRRPC-----HGEKGTAKGCLCERLRYLVSLACVCVPRV 175  
 Db 100 -GAVD--YHNSNVPYIQOELLVYKRGHQPCNSRLEKML--YVAGTCVCTPIY 147

```

1      RESULT 10
2      US-09-022-696-8
3      : Sequence 8, Application US/09022696
4      : Patent No. 6072037
5      : GENERAL INFORMATION:
6      : APPLICANT: Yao, Zhenqin
7      : APPLICANT: Spriggs, Melanie
8      : APPLICANT: Fanslow, William
9      : TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
10     : NUMBER OF SEQUENCES: 10
11     : CORRESPONDENCE ADDRESS:
12     : ADDRESSEE: ImmuneX Corporation
13     : STREET: 51 University Street
14     : CITY: Seattle
15     : STATE: WA
16     : COUNTRY: USA
17     : ZIP: 98101
18     : COMPUTER READABLE FORM:
19     : MEDIUM TYPE: Floppy disk
20     : COMPUTER: Apple Power Macintosh
21     : OPERATING SYSTEM: Apple Operating System 7.5.5
22     : SOFTWARE: Microsoft Word for Apple, Version 6.0.1
23     : CURRENT APPLICATION DATA:
24     : APPLICATION NUMBER: US/09/022, 696
25     : FILING DATE:
26     : CLASSIFICATION:
27     : PRIORITY APPLICATION DATA:
28     : APPLICATION NUMBER: 08/620, 694
29     : FILING DATE:
30     : CLASSIFICATION:
31     : PRIORITY APPLICATION DATA:
32     : APPLICATION NUMBER: USSN 08/410, 535
33     : FILING DATE: 23 MARCH 1995
34     : CLASSIFICATION:
35     : ATTORNEY/AGENT INFORMATION:
36     : NAME: Perkins, Patricia Anne
37     : REGISTRATION NUMBER: 34, 695
38     : REFERENCE/DOCKET NUMBER: 2617-B
39     : TELECOMMUNICATION INFORMATION:
40     : TELEPHONE: (206)567-0430
41     : TELEFAX: (206)
42     : INFORMATION FOR SEQ ID NO: 8:
43     : SEQUENCE CHARACTERISTICS:
44     : LENGTH: 151 amino acids
45     : TYPE: amino acid
46     : STRANDEDNESS: not relevant
47     : TOPOLOGY: linear
48     : MOLECULE TYPE: protein
49     : HYPOTHEetical: NO
50     : ANTI-SENSE: NO
51     : ORIGINAL SOURCE:
52     : ORGANISM: Herpesvirus Saimiri
53     : STRAIN: ORF13
54     : US-09-022-696-8

```

Query Match	9.5%	Score 93.5;	DB 3;	Length 151;
Best Local Similarity	23.0%;	Pred. No. 0.009;		
Matches 40;	Conservative 28;	Mismatches 65;	Indels 41;	Gaps 8;



OY 11 SSLISLFLQVAVFLAMVGTHTYSHMPCSCPSKGDTSSELL-----RMSVVPVPLEPA 65  
Best Local Similarity 23.0%; Pred. No. 0.009; Length 151;  
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;  
DB 6 TSLVLL--LSDICVYKSETTSAGTPRCLAANSPFRSVAWVTLISRNMT-----54  
OY 66 RPNRHPSCRASDGPLNSRAISPMRYELDRDLNRLPDLYHARCCLPHCVSLQTSQSHMD 125  
DB 55 -----SSKRASD---YNNRSTSPWTLHRNEDQDRYPSVIMEAKRCVLCGVNAD-----99  
OY 126 PRGNSELYHNQVYFRRPC-----HGEKGTHKGYCLERRLYRVSILACVCPVPRV 175  
DB 100 --GNVD--YHMSVPIQOEILVVRKGHQPSPNFRLEKML--VTVCCTCVPPIV 147

RESULT 11  
US-08-685-239-6  
Sequence 6, Application US/08685239  
Patent No. 6074849  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlio, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Piltman, Debra  
APPLICANT: Ml, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, Joann  
APPLICANT: Golden/Fleet, Margaret  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,239  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION/DOCKET NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-239-6

Query Match 9.5%; Score 93.5; DB 3; Length 151;  
Best Local Similarity 23.0%; Pred. No. 0.009;  
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;  
OY 11 SSLISLFLQVAVFLAMVGTHTYSHMPCSCPSKGDTSSELL-----RMSVVPVPLEPA 65  
DB 6 TSLVLL--LSDICVYKSETTSAGTPRCLAANSPFRSVAWVTLISRNMT-----54  
OY 66 RPNRHPSCRASDGPLNSRAISPMRYELDRDLNRLPDLYHARCCLPHCVSLQTSQSHMD 125  
DB 55 -----SSKRASD---YNNRSTSPWTLHRNEDQDRYPSVIMEAKRCVLCGVNAD-----99  
OY 126 PRGNSELYHNQVYFRRPC-----HGEKGTHKGYCLERRLYRVSILACVCPVPRV 175

DB 100 --GNVD--YHMSVPIQOEILVVRKGHQPSPNFRLEKML--VTVCCTCVPPIV 147

RESULT 12  
US-09-022-253-8  
Sequence 8, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spilgus, William  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION/DOCKET NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: NO  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-253-8

Query Match 9.5%; Score 93.5; DB 3; Length 151;  
Best Local Similarity 23.0%; Pred. No. 0.009;  
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;  
OY 11 SSLISLFLQVAVFLAMVGTHTYSHMPCSCPSKGDTSSELL-----RMSVVPVPLEPA 65  
DB 6 TSLVLL--LSDICVYKSETTSAGTPRCLAANSPFRSVAWVTLISRNMT-----54  
OY 66 RPNRHPSCRASDGPLNSRAISPMRYELDRDLNRLPDLYHARCCLPHCVSLQTSQSHMD 125  
DB 55 -----SSKRASD---YNNRSTSPWTLHRNEDQDRYPSVIMEAKRCVLCGVNAD-----99

OY 126 PRGNSELYHNOTVYFRPC---HGEKTHKGYCLERLYRSLACVCPRV 175  
DB 100 --GNDV--YHNSVPIQOEILVVRKGHOPCPNSFRLKML--VTVGCTVTPIV 147

## RESULT 13

US-09-022-260-8  
Sequence 8, Application US/09022260  
Patent No. 6100235  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6100235e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US98 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
SPRAIN: ORF13  
US-09-022-260-8

Query Match 9.5%; Score 93.5; DB 3; Length 151;  
Best Local Similarity 23.0%; Pred. No. 0.009;  
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

OY 11 SLSISFLQVAVFLAMVMTHTYSHWPCPSKGGDTSEEL-----RWSTVPVPLEPA 65  
DB 6 TSLVLL--LSIDICIVSEITSAGTPCLANNSPRSVMYTLIRNMWT----- 54  
OY 66 RPNRHPESCRASEDPLNSAISPMRYELDRDLNRLPDLYHARCCLPHCVSLQTGSHMD 125  
DB 55 -----SSKRAD---YNNRSTSPMTLHNRNEDODRTPSVIWEAKCRYLGCNVND----- 99  
OY 126 PRGNSELYHNOTVYFRPC---HGEKTHKGYCLERLYRSLACVCPRV 175

DB 100 --GNDV--YHNSVPIQOEILVVRKGHOPCPNSFRLKML--VTVGCTVTPIV 147

## RESULT 14

US-09-022-259-8  
Sequence 8, Application US/09022259  
Patent No. 6191104  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6191104e1 Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,259  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US98 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
SPRAIN: ORF13  
US-09-022-259-8

Query Match 9.5%; Score 93.5; DB 4; Length 151;  
Best Local Similarity 23.0%; Pred. No. 0.009;  
Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

OY 11 SLSISFLQVAVFLAMVMTHTYSHWPCPSKGGDTSEEL-----RWSTVPVPLEPA 65  
DB 6 TSLVLL--LSIDICIVSEITSAGTPCLANNSPRSVMYTLIRNMWT----- 54  
OY 66 RPNRHPESCRASEDPLNSAISPMRYELDRDLNRLPDLYHARCCLPHCVSLQTGSHMD 125  
DB 55 -----SSKRAD---YNNRSTSPMTLHNRNEDODRTPSVIWEAKCRYLGCNVND----- 99  
OY 126 PRGNSELYHNOTVYFRPC---HGEKTHKGYCLERLYRSLACVCPRV 175

Db 100 --GNVD--YHMNSVPIQOELLVVRKHQPCPNFRLKML--VTGCGCTVTPIV 147

## RESULT 15

US-09-022-257-8

; Sequence 8, Application us/09022257  
; Patent No. 6197525

## GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

TITLE OF INVENTION: No. 6197525el Receptor that binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,257

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USN 08/410,535

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 151 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Herpesvirus Saimiri

STRAIN: ORF13

US-09-022-257-8

## Query Match

Best local Similarity 9.5%; Score 93.5; DB 4; Length 151;

Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;

QY 11 SLSISLFQVAVFLAMVGTHTYSHMPSCPSKQDTSSELL-----RMSTVPVPPLEPA 65

Db 6 TSLVLLLL--LSIDCIYKSETSAQTPCLANNSFPRSVMTLSIRMMNT----- 54

QY 66 RPNHRPSCASAEQDPLNSRAISPMRELDRLNRLPDQLYHARCLCPHCVSLQTSQSHMD 125

Db 55 -----SKRRSD--YNNRSTSPMTLARNEDQDRYPSVINEAKCRYLGCVNAD----- 99

QY 126 PRGNSELLYNQTVFYRRPC---HGEKGTAKGYCLERRLYRVSLACVCPVRPV 175

Db 100 --GNVD--YHMNSVPIQOELLVVRKHQPCPNFRLKML--VTGCGCTVTPIV 147

Search completed: February 26, 2003, 09:33:48  
Job time : 15 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:31:56 ; Search time 14 Seconds

(Without alignments)  
476.912 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985

Sequence: 1 MRRPRLEGSLSLIFLQY.....ERRLYRVSLACVAPRYWG 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174566 seqs, 37721826 residues

Total number of hits satisfying chosen parameters: 174566

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_Aa:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCR\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	985	100.0	177	9	US-09-874-503-6
2	985	100.0	177	9	US-10-000-157-6
3	985	100.0	177	9	US-10-063-547-156
4	985	100.0	177	9	US-09-816-744-6
5	985	100.0	177	9	US-09-747-259-6
6	985	100.0	177	9	US-10-063-616-156
7	985	100.0	177	9	US-10-063-502-156
8	985	100.0	177	12	US-10-006-867-156
9	898	91.2	161	10	US-09-886-404-2
10	697	70.8	169	10	US-09-886-404-4
11	670	68.0	159	10	US-09-886-404-10
12	170.5	17.3	206	10	US-09-854-280-24
13	170.5	17.3	206	10	US-09-854-208-24
14	165.5	16.8	197	9	US-09-874-503-4
15	165.5	16.8	197	9	US-10-000-157-4
16	165.5	16.8	197	9	US-10-036-041-11
17	165.5	16.8	197	9	US-09-320-713-29
18	165.5	16.8	197	9	US-09-816-744-4
19	165.5	16.8	197	9	US-09-747-259-4

#### ALIGNMENTS

RESULT 1  
US-09-874-503-6  
Sequence 6, Application US/09874503  
Patent No. US20020177188A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hymowitz, Sarah G.  
APPLICANT: Tumias, Daniel  
APPLICANT: Starovashnik, Melissa A.  
APPLICANT: VanLooken, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C1P3(US)  
CURRENT APPLICATION NUMBER: US/09/874,503  
CURRENT FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 60/138,387

20	165.5	16.8	197	9	US-10-035-855-11	Sequence 11, Appl
21	165.5	16.8	197	9	US-10-174-550-448	Sequence 448, App
22	165.5	16.8	197	9	US-10-176-758-448	Sequence 448, App
23	165.5	16.8	197	9	US-10-175-737-448	Sequence 448, App
24	165.5	16.8	197	9	US-10-173-706-448	Sequence 448, App
25	165.5	16.8	197	9	US-10-175-738-448	Sequence 448, App
26	165.5	16.8	197	9	US-10-175-752-448	Sequence 448, App
27	165.5	16.8	197	9	US-10-176-482-448	Sequence 448, App
28	165.5	16.8	197	9	US-10-176-757-448	Sequence 448, App
29	165.5	16.8	197	9	US-10-176-913-448	Sequence 448, App
30	165.5	16.8	197	9	US-10-180-552-448	Sequence 448, App
31	165.5	16.8	197	9	US-10-180-552-448	Sequence 448, App
32	165.5	16.8	197	9	US-09-931-836-111	Sequence 11, Appl
33	165.5	16.8	197	9	US-10-173-700-448	Sequence 448, App
34	165.5	16.8	197	9	US-10-174-572-448	Sequence 448, App
35	165.5	16.8	197	9	US-10-174-579-448	Sequence 448, App
36	165.5	16.8	197	9	US-10-174-582-448	Sequence 448, App
37	165.5	16.8	197	9	US-10-175-739-448	Sequence 448, App
38	165.5	16.8	197	9	US-10-175-740-448	Sequence 448, App
39	165.5	16.8	197	9	US-10-175-743-448	Sequence 448, App
40	165.5	16.8	197	9	US-10-176-488-448	Sequence 448, App
41	165.5	16.8	197	9	US-10-176-492-448	Sequence 448, App
42	165.5	16.8	197	9	US-10-176-747-448	Sequence 448, App
43	165.5	16.8	197	9	US-10-176-750-448	Sequence 448, App
44	165.5	16.8	197	9	US-10-176-985-448	Sequence 448, App
45	165.5	16.8	197	9	US-10-176-985-448	Sequence 448, App

PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: US 60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: US 60/130,232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: US 60/113,621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-20  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: US 09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: US PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: US PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: US PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US99/05028  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 6  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-874-503-6

Query Match 100.0%; Score 985; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4,1e-85;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRPRLGDSLSILFLQVVAFLAMVGTHTYSHMPSCCPKSGODTSEELLRKSTVPVP 60  
DB 1 MRRPRLGDSLSILFLQVVAFLAMVGTHTYSHMPSCCPKSGODTSEELLRKSTVPVP 60  
QY 61 PLEPARPNHPPSCRASEGGPLNSRAISPMRYELDRDLNLPDLYHARCLCPHCVSLQT 120  
DB 61 PLEPARPNHPPSCRASEGGPLNSRAISPMRYELDRDLNLPDLYHARCLCPHCVSLQT 120  
QY 121 GSHMPRGNSSELLYHNGTYFYRRPCHGKGTGKGYCLERLRYSLACVCRPRVWG 177

DB 121 GSHMPRGNSSELLYHNGTYFYRRPCHGKGTGKGYCLERLRYSLACVCRPRVWG 177

RESULT 2  
US-10-000-157-6  
Sequence 6, Application US/10000157  
Publication No. US20020182673A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul L.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hymowitz, Sarah  
APPLICANT: Tamas, Daniel  
APPLICANT: Starovassnik, Melissa.  
APPLICANT: Vanlookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Matanabe, Collin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
TITLE OR INVENTION: IT-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381AC1P4(US)  
CURRENT APPLICATION NUMBER: US/10/000,157  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/130232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: 60/131022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: 60/134287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/172096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/213807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: 60/242837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: 60/244072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: 60/253646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/644848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: 09/747259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 09/816744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: 09/854208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: 09/854280  
PRIOR FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 09/874503  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: 09/908827  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 09/929404  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 09/931836  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: PCT/US99/05028  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: PCT/US99/10733  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: PCT/US99/31274  
PRIOR FILING DATE: 1999-12-30  
PRIOR APPLICATION NUMBER: PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/US00/05601  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: PCT/US00/15264  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/17800  
PRIOR FILING DATE: 2001-06-01  
PRIOR APPLICATION NUMBER: PCT/US01/19692  
PRIOR FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: PCT/US01/21066  
PRIOR FILING DATE: 2001-06-29  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 6  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-000-157-6

Query Match 100.0%; Score 985; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4; Le-85;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRERPRGDSLSISLFQVAVFLAMVGTHTYSHMPCSCPSKGGDTSEELLRMSTVYP 60  
DB 1 MRERPRGDSLSISLFQVAVFLAMVGTHTYSHMPCSCPSKGGDTSEELLRMSTVYP 60  
QY 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSLOT 120  
DB 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSLOT 120  
QY 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGKGTGKGYCLERRLRYVSLACVCPRPVWG 177  
DB 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGKGTGKGYCLERRLRYVSLACVCPRPVWG 177

RESULT 3  
US-10-063-547-156  
Sequence 156, Application US/10063547  
Publication No. US20020182638A1  
GENERAL INFORMATION:

APPLICANT: Eaton, Dan L.  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey J.  
APPLICANT: Goddard, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT APPLICATION NUMBER: US/10/063,547  
CURRENT FILING DATE: 2002-05-02  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 156  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-547-156

Query Match 100.0%; Score 985; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4; Le-85;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRERPRGDSLSISLFQVAVFLAMVGTHTYSHMPCSCPSKGGDTSEELLRMSTVYP 60  
DB 1 MRERPRGDSLSISLFQVAVFLAMVGTHTYSHMPCSCPSKGGDTSEELLRMSTVYP 60  
QY 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSLOT 120  
DB 61 PLEPARPNRHPESCRASEDEGPLNSRAISPMRYELDRDLNRLPQDLYHACCLCPHCVSLOT 120  
QY 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGKGTGKGYCLERRLRYVSLACVCPRPVWG 177  
DB 121 GSHMDPRGNSSELLYHNOTVFFRRPCHGKGTGKGYCLERRLRYVSLACVCPRPVWG 177

RESULT 4  
US-09-816-744-6  
Sequence 6, Application US/09816744  
Publication No. US20030003546A1  
GENERAL INFORMATION:

APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Goddard, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth  
APPLICANT: Tumas, Daniel  
APPLICANT: Vanlookeren, Manno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
FILE REFERENCE: P1381R1C1P2(US)  
CURRENT APPLICATION NUMBER: US/09/816,744  
CURRENT FILING DATE: 2001-03-22  
Prior application data removed - consult PALM or file wrapper  
NUMBER OF SEQ ID NOS: 39  
SEQ ID NO 6  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-816-744-6

Query Match 100.0%; Score 985; DB 9; Length 177;

PRIOR FILING DATE: 2000-11-28

Publication No. US20030023042A1



GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvarsoff, Ellen  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gutney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT FILING DATE: 2002-05-01  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 170  
SEQ ID NO 156  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-063-502-156

Query Match 100.0%; Score 985; DB 9; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.1e-85;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRERPRLEDESSLSLFLQVAVAFAMVWGTHTYSHWPCSCPSKGDTSSELLRMSTVVP 60  
DB 1 MRERPRLEDESSLSLFLQVAVAFAMVWGTHTYSHWPCSCPSKGDTSSELLRMSTVVP 60  
QY 61 PLEPRARPRHSPESCRASEDGLPNSRAISPMRYELDRDINRLPQDLYHARCLOPHCVSLQ 120  
DB 61 PLEPRARPRHSPESCRASEDGLPNSRAISPMRYELDRDINRLPQDLYHARCLOPHCVSLQ 120  
QY 121 GSHMDPRGNSSELYNQVTFYRPPCHGEGTKGKGYCLERLYRVSILACYVPRVWG 177  
DB 121 GSHMDPRGNSSELYNQVTFYRPPCHGEGTKGKGYCLERLYRVSILACYVPRVWG 177

RESULT 8  
US-10-006-867-156  
Sequence 156, Application US/10006867  
Patent No. US20020119130A1  
GENERAL INFORMATION:  
APPLICANT: Eaton, Dan L.  
APPLICANT: Filvarsoff, Ellen  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gutney, Austin L.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3230R1C1  
CURRENT FILING DATE: 2001-12-06  
CURRENT APPLICATION NUMBER: US/10/006, 867  
PRIOR APPLICATION NUMBER: 60/064215  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088740  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088811  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088825  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088863  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089553  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090688  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091628  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/096012  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096757  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/096949  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/096959  
PRIOR FILING DATE: 1998-08-18  
PRIOR APPLICATION NUMBER: 60/097954  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097971  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/097979  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101279

PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102570  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/103449  
PRIOR FILING DATE: 1998-10-06  
PRIOR APPLICATION NUMBER: 60/103678  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103679  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/103711  
PRIOR FILING DATE: 1998-10-08  
PRIOR APPLICATION NUMBER: 60/105000  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105002  
PRIOR FILING DATE: 1998-10-20  
PRIOR APPLICATION NUMBER: 60/105881  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: 60/106030  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106856  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108807  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/112419  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/112853  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113011  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/112854  
PRIOR FILING DATE: 1998-12-16  
PRIOR APPLICATION NUMBER: 60/113300  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113408  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113430  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/114223  
PRIOR FILING DATE: 1998-12-30  
PRIOR APPLICATION NUMBER: 60/115614  
PRIOR FILING DATE: 1999-01-17  
PRIOR APPLICATION NUMBER: 60/115527  
PRIOR FILING DATE: 1999-01-20  
PRIOR APPLICATION NUMBER: 60/116843  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: 60/119285  
PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/119287  
PRIOR FILING DATE: 1999-02-09  
PRIOR APPLICATION NUMBER: 60/119525  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/120014  
PRIOR FILING DATE: 1999-02-11  
PRIOR APPLICATION NUMBER: 60/129122  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 60/129674  
PRIOR FILING DATE: 1999-04-16

PRIOR APPLICATION NUMBER: 60/131291  
PRIOR FILING DATE: 1999-04-27  
PRIOR APPLICATION NUMBER: 60/138387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: 60/144791  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/169495  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/175481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: 60/191007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/199397  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: 09/380139  
PRIOR FILING DATE: 1998-08-25  
PRIOR APPLICATION NUMBER: 09/311832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 09/380137  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: 09/380142

Query Match 100.0%; Score 985; DB 12; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4, 1e-85;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRPRLGESSLSIFLQVVAFLAMVGTHTYSHMPSCCPKGGDTSELLRMSTVPVP 60  
DB 1 MRRPRLGESSLSIFLQVVAFLAMVGTHTYSHMPSCCPKGGDTSELLRMSTVPVP 60  
QY 61 PLEPARPNRHPSCSEGCPLNSRAISPMRYELDRDLRLPDDLYHARGLCPHCYSLOT 120  
DB 61 PLEPARPNRHPSCSEGCPLNSRAISPMRYELDRDLRLPDDLYHARGLCPHCYSLOT 120  
QY 121 GSHMDRGNSLLYHNGTVFYRRPCHGCKTHKGYCLERLYVSLACVVRPVWG 177  
DB 121 GSHMDRGNSLLYHNGTVFYRRPCHGCKTHKGYCLERLYVSLACVVRPVWG 177

## RESULT 9

US-09-886-404-2

Sequence 2, Application US/09886404

Patent No. US2002003752A1

GENERAL INFORMATION: Eugene

APPLICANT: Medlock, Eugene

APPLICANT: Yeh, Richard

APPLICANT: Silbiger, Scott M.

APPLICANT: Elliott, Gary S.

APPLICANT: Nguyen, Hung Q.

APPLICANT: Jing, Shugian

TITLE OF INVENTION: IL-17 Like Molecules and Uses thereof

FILE REFERENCE: 01017/37128B

CURRENT APPLICATION NUMBER: US/09/886,404

PRIOR FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: 09/810,384

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/266,159

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 60/213,125

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 60/213,125

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 161

TYPE: PRT

ORGANISM: Homo sapiens

US-09-886-404-2

Query Match 91.2%; Score 898; DB 10; Length 161;  
Best Local Similarity 100.0%; Pred. No. 5e-77; Indels 0; Gaps 0;  
Matches 159; Conservative 0; Mismatches 0;

QY 19 QVAFLLAMVGTHTYTHSHMPSCPSKQDTSSELLRWSTVPPVPLEPARNHPESCRASE 78  
 DB 3 QVAFLLAMVGTHTYTHSHMPSCPSKQDTSSELLRWSTVPPVPLEPARNHPESCRASE 62  
 QY 79 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCPCVSLQSGHMDRGNSELLYHNO 138  
 DB 63 DGPLNSRAISPMRYELDRDLNRLPQDLYHARCPCVSLQSGHMDRGNSELLYHNO 122  
 QY 139 VFYRRPCHGEKGTTHKGYCLERLRYVSLACVCPRRVNG 177  
 DB 123 VFYRRPCHGEKGTTHKGYCLERLRYVSLACVCPRRVNG 161

RESULT 10  
 US-09-886-404-4  
 ; Sequence 4, Application US/09886404  
 ; Patent No. US20020037524A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Medlock, Eugene  
 ; APPLICANT: Yeh, Richard  
 ; APPLICANT: Silbiger, Scott M.  
 ; APPLICANT: Elliot, Gary S.  
 ; APPLICANT: Nguyen, Hung Q.  
 ; APPLICANT: Jiny, Shuguan  
 ; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof  
 ; FILE REFERENCE: 01017/37128B  
 ; CURRENT APPLICATION NUMBER: US/09/886,404  
 ; PRIOR FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: 09/810,384  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/266,159  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: 60/213,125  
 ; PRIOR FILING DATE: 2000-06-22  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 4  
 ; LENGTH: 169  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-886-404-4

Query Match 70.8%; Score 697; DB 10; Length 169;  
 Best Local Similarity 76.5%; Pred. No. 3.4e-58;  
 Matches 127; Conservative 9; Mismatches 22; Indels 8; Gaps 1;

QY 19 QVAFLLAMVGTHTYTHSHMPSCPSKQDTSSELLRWSTVPPVPLEPARNHPESCRASE 78  
 DB 3 QVAFLLAMVGTHTYTHSHMPSCPSKQDTSSELLRWSTVPPVPLEPARNHPESCRASE 62  
 QY 71 PESCRASEDEPLNSRAISPMRYELDRDLNRLPQDLYHARCPCVSLQSGHMDRGNSELLYHNO 130  
 DB 63 AESCRASKDGPLNSRAISPMRYELDRDLNRLPQDLYHARCPCVSLQSGHMDRGNSELLYHNO 122  
 QY 131 ELLYHNOVFYRRPCHGEKGTTHKGYCLERLRYVSLACVCPRRVNG 176  
 DB 123 VPLYNQVYRRPCHGEKGTTHKGYCLERLRYVSLACVCPRRVNG 168

RESULT 11  
 US-09-886-404-10  
 ; Sequence 10, Application US/09886404  
 ; Patent No. US20020037524A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Medlock, Eugene  
 ; APPLICANT: Yeh, Richard  
 ; APPLICANT: Silbiger, Scott M.  
 ; APPLICANT: Elliot, Gary S.  
 ; APPLICANT: Nguyen, Hung Q.  
 ; APPLICANT: Jiny, Shuguan  
 ; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof  
 ; FILE REFERENCE: 01017/37128B

CURRENT APPLICATION NUMBER: US/09/886,404  
 ; CURRENT FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: 09/810,384  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/266,159  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: 60/213,125  
 ; PRIOR FILING DATE: 2000-06-22  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 159  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 US-09-886-404-10

Query Match 68.0%; Score 670; DB 10; Length 159;  
 Best Local Similarity 76.1%; Pred. No. 1.1e-55;  
 Matches 121; Conservative 9; Mismatches 21; Indels 8; Gaps 1;

QY 26 NVMGTHYTHSHMPSCPSKQDTSSELLRWSTVPPVPLEPARNHPESCRASE 77  
 DB 1 NVMGTHYTHSHMPSCPSKQDTSSELLRWSTVPPVPLEPARNHPESCRASE 60  
 QY 78 EDGPLNSRAISPMRYELDRDLNRLPQDLYHARCPCVSLQSGHMDRGNSELLYHNO 137  
 DB 61 KGPLNSRAISPMRYELDRDLNRLPQDLYHARCPCVSLQSGHMDRGNSELLYHNO 120  
 QY 138 TVYRRPCHGEKGTTHKGYCLERLRYVSLACVCPRRVNG 176  
 DB 121 TVYRRPCHGEKGTTHKGYCLERLRYVSLACVCPRRVNG 159

RESULT 12  
 US-09-854-280-24  
 ; Sequence 24, Application US/09854280  
 ; Patent No. US20020052027A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Gurney, Austin  
 ; APPLICANT: Li, Hanzhong  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
 ; FILE REFERENCE: P1381R1C2  
 ; CURRENT APPLICATION NUMBER: US/09/854,280  
 ; CURRENT FILING DATE: 2001-05-10  
 ; PRIOR APPLICATION NUMBER: US 09/311,832  
 ; PRIOR FILING DATE: 1999-05-14  
 ; PRIOR APPLICATION NUMBER: US 60/085,579  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: US 60/113,621  
 ; PRIOR FILING DATE: 1998-12-23  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SEQ ID NO 24  
 ; LENGTH: 206  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: IL-17C-His tag  
 US-09-854-280-24

Query Match 17.3%; Score 170.5; DB 10; Length 206;  
 Best Local Similarity 29.8%; Pred. No. 7.8e-09;  
 Matches 53; Conservative 17; Mismatches 71; Indels 37; Gaps 7;  
 QY 31 HTYSHMPSCPSKQDTSSELLRWSTVPPVPLEPARNHPESCRASE 73  
 DB 27 HPHSHGTPHCYS-----ABELPLGQAPHLARGAKWGQALVALVSLAASHNGRHR 81  
 QY 74 CRASEDGPL-----NSRAISPMRYELDRDLNRLPQDLYHARCPCVSLQSGHMDRGNSELLYHNO 122

Db 82 PSATGCPVLRPEEVLADTHORSISPMWRYVDTEDEYPOKLAFAECLRGCIDARTGR 141  
QY 123 HMDPGNSSELYNQVYFRRPCHGKENG---THKGYCLERLRYSLACVCPRVWG 177  
Db 142 ETAAL-NSVALLQSLVLRRRRPSRDSGLPTGAFHTEFTHVPGCTCVPFRSNG 198

RESULT 13  
US-09-854-208-24  
Sequence 24, Application US/09854208  
Patent No. US20020106743A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Goddard, Audrey  
APPLICANT: Guiney, Austin  
APPLICANT: Li, Hanzhong  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: P1381-R1  
CURRENT APPLICATION NUMBER: US/09/854,208  
CURRENT FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US/09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: US 60/113,621  
PRIOR FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 26  
SEQ ID NO 24  
LENGTH: 206  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: Artificial sequence  
LOCATION: 1-206  
OTHER INFORMATION: IL-17C-His tag  
US-09-854-208-24

Query Match 17.3%; Score 170.5; DB 10; Length 206;  
Best Local Similarity 29.8%; Pred. No. 7, 8e-09;  
Matches 53; Conservative 17; Mismatches 71; Indels 37; Gaps 7;

QY 31 HYSHPSCPSKSGQDTSEEL-----LW-STVP---VPLEPARNRHPS 73  
Db 27 HPHSGTPIGYS-----AEELPLGQAPPHLLARGAMGGLPVALYSSLEAASHRGHNR 81  
QY 74 CRASEDGPL-----NSRAISPMWRYELDRDLNRLPQDLYHARCICPHCVSLQTS 122  
Db 82 PSATGCPVLRPEEVLADTHORSISPMWRYVDTEDEYPOKLAFAECLRGCIDARTGR 141  
QY 123 HMDPGNSSELYNQVYFRRPCHGKENG---THKGYCLERLRYSLACVCPRVWG 177  
Db 142 ETAAL-NSVALLQSLVLRRRRPSRDSGLPTGAFHTEFTHVPGCTCVPFRSNG 198

RESULT 14  
US-09-874-503-4  
Sequence 4, Application US/09874503  
Patent No. US20020177188A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Jian  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Li, Hanzhong  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Hymowitz, Sarah G.  
APPLICANT: Tumas, Daniel

APPLICANT: Starovasanik, Melissa A.  
APPLICANT: Vanlookeren, Menno  
APPLICANT: Vandlen, Richard  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Yansura, Daniel  
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF  
TITLE OF INVENTION: P1381R1C1P3(US)  
FILE REFERENCE: P1381R1C1P3(US)  
CURRENT APPLICATION NUMBER: US/09/874,503  
CURRENT FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/253,646  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: US 60/244,072  
PRIOR FILING DATE: 2000-10-26  
PRIOR APPLICATION NUMBER: US 60/242,837  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/175,481  
PRIOR FILING DATE: 2000-01-11  
PRIOR APPLICATION NUMBER: US 60/191,007  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US 60/213,807  
PRIOR FILING DATE: 2000-06-22  
PRIOR APPLICATION NUMBER: US 60/172,096  
PRIOR FILING DATE: 1999-12-23  
PRIOR APPLICATION NUMBER: US 60/138,387  
PRIOR FILING DATE: 1999-06-09  
PRIOR APPLICATION NUMBER: US 60/134,287  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US 60/131,022  
PRIOR FILING DATE: 1999-04-26  
PRIOR APPLICATION NUMBER: US 60/130,232  
PRIOR FILING DATE: 1999-04-21  
PRIOR APPLICATION NUMBER: US 60/113,621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: US 60/085,579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-20  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/644,848  
PRIOR FILING DATE: 2000-08-22  
PRIOR APPLICATION NUMBER: US 09/380,142  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/380,138  
PRIOR FILING DATE: 1999-08-25  
PRIOR APPLICATION NUMBER: US 09/311,832  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: US PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: US PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: US PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US PCT/US00/15364  
PRIOR FILING DATE: 2000-06-02  
PRIOR APPLICATION NUMBER: US PCT/US00/07532  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: US PCT/US00/05841  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US PCT/US00/05601  
PRIOR FILING DATE: 2000-03-01  
PRIOR APPLICATION NUMBER: US PCT/US00/04341  
PRIOR FILING DATE: 2000-02-18

[illegible]

SEQ ID NO 4  
LENGTH: 197

TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-000-157-4

Query Match 16.8%; Score 165.5; DB 9; Length 197;  
Best Local Similarity 29.7%; Pred. No. 2.2e-08;  
Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;

```

OY 31 HTYSHMPSCCPKSGQDTSEEL-----LRW-STVP---VPLEPARPNRHPES 73
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 27 HPHSHGTPHCYS-----AELPLGQAPPHLARGAKWGQALPVALVSSLEASHRGHRER 81
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 74 CRASEDDGPL-----NSRAISPMRYELDRDLNRLPQDLYHARCLCPHCVSLOTGS 122
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 82 PSATTOCPVLRPEVLEADTHQRSISPWRIVYDDEDRYPQKLAFAECLCRGCIIDARTGR 141
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
OY 123 HMDPRGNSELLYHNOTVYFRRPCHGEGK---THKGYCLERLYRYSLACVYRPR 174
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 142 ETVAL-NSVRLQSLVLRPRPCSRDGSGLPTPGAFAFHTEFIHVPVGCCTVLPFR 195
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

Search completed: February 26, 2003, 09:34:08  
Job time : 15 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:30:41 ; Search time 46 Seconds  
(without alignments)  
369.909 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985  
Sequence: 1 MRRPRRGEDSLISLFLQY.....ERRLYRVSLACVVRPMVG 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	10.9	162	T32515	hypothetical prote
2	93.5	9.5	151	B45351	immediate-early pr
3	91	9.2	150	I49623	cytotoxic T-lympho
4	88.5	9.0	422	A60503	sperm-binding glyco
5	86	8.7	147	JC4628	cytotoxic T-lympho
6	83	8.4	1323	I78557	N-methyl-D-asparta
7	81.5	8.3	467	A47388	serine/threonine p
8	78.5	8.0	206	T25139	hypothetical prote
9	78	7.9	358	J00805	thrombospondin 4 p
10	77.5	7.9	961	I7SHD4	hypothetical prote
11	77	7.8	263	I48742	hydrogenase (EC 1.
12	77	7.8	344	I11776	N-methyl-D-asparta
13	76.5	7.7	1323	S27224	hypothetical prote
14	75.5	7.7	446	G85064	hypothetical prote
15	75.5	7.7	898	T14764	SH2-containing ino
16	75.5	7.7	1189	JC6118	gastric mucin MUC5
17	74.5	7.6	850	S56015	DNA topoisomerase
18	74.5	7.6	892	T06818	telomerase catalyt
19	74.5	7.6	1132	T03844	adenosine deaminas
20	74.5	7.6	1175	I57549	structural polypro
21	74.5	7.6	1254	J01978	gastric mucin MUC5
22	74.5	7.6	1373	J05095	DNA (cytosine-5)-
23	74.5	7.6	1612	JC5210	hypothetical prote
24	74	7.5	237	A40672	ADAM 6 protein pre
25	73.5	7.5	735	I48101	collagen alpha 1(X
26	73	7.4	482	B31795	GPI protein - mous
27	72.5	7.4	1840	T30250	insulin-like growt
28	72.5	7.4	240	A39842	hypothetical prote
29	72.5	7.4	294	T34537	hypothetical prote

30	72.5	7.4	419	2	T19871	hypothetical prote
31	72.5	7.4	602	2	H70796	hypothetical prote
32	72.5	7.4	1188	2	JC4889	phosphatidylinosit
33	72.5	7.4	1254	1	J01979	structural polypro
34	72.5	7.4	3744	2	S46715	hypothetical prote
35	72	7.3	216	2	T30657	hypothetical prote
36	72	7.3	238	2	T48605	insulin-like growt
37	72	7.3	360	1	S11968	hydrogenase (EC 1.
38	72	7.3	391	2	JC6193	tumor suppressor p
39	72	7.3	1348	2	S27812	probable epidermal
40	72	7.3	1348	2	A43917	hypothetical prote
41	71.5	7.3	166	2	C72734	hypothetical prote
42	71.5	7.3	650	2	AB2004	hypothetical prote
43	71.5	7.3	2319	2	A47004	coagulation factor
44	71	7.2	488	2	S13423	stromelysin 3 (EC
45	71	7.2	530	2	T30505	hypothetical prote

## ALIGNMENTS

## RESULT 1

T32515  
hypothetical protein C44B12.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C:Accession: T32515

R:Titin-Wollam, A.

A:Submitted to the EMBL Data Library, December 1997

A:Description: The sequence of C. elegans cosmid C44B12.

A:Reference number: Z21183

A:Accession: T32515

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-162 <PIN>

A:Cross-references: EMBL:AF036692; PIDN:AA88329.1; GSPDB:GND00022; CESP:C44B12.6

A:Experimental source: strain Bristol N2; clone C44B12

A:Gene: CESP:C44B12.6

A:Map position: 4

A:Introns: 41/3; 95/3; 115/1

Query Match

Best Local Similarity 26.2%; Pred. No. 0.011;

Matches 34; Conservative

Mismatches 39; Indels 34; Gaps 6;

Db

43 KGDTSELLRMSTVPVPLEPARPNRHPESCRASEDGLNSRAISPMRYELDRDLNRLP 102

57 KSRDCSEPSIDKSEVLP-----DQPLSERSTCPYHHLNLYDKRRIP 98

103 QDLVHARCLCPHCVSIDTG-SHMDPRGNSSELLYHQVYFRRPCHGEYTHKGYCLERRL 161

99 AAISEVSCSPH-VKVGHGIIHCEP-----MMYNMRVWLFDDSC--DK-----YVERV 143

162 YRVSLACV 171

144 QKVALACV 153

Db

162 YRVSLACV 171

144 QKVALACV 153

Db

162 YRVSLACV 171

144 QKVALACV 153

Db

162 YRVSLACV 171

144 QKVALACV 153

Db

162 YRVSLACV 171

144 QKVALACV 153

Db

162 YRVSLACV 171

144 QKVALACV 153

Db

162 YRVSLACV 171

144 QKVALACV 153



A:Residues: 1-151 <NIN>  
 A:Cross-references: GB:M60286; NID:9331040; PIDN:AAA6156.1; PID:9331042  
 R:Albrecht, J.  
 Submitted to the EMBL Data Library, January 1992  
 A:Description: Primary structure of the herpesvirus saimiri genome.  
 A:Accession number: A36806  
 A:Reference number: D36807  
 A:Accession type: DNA  
 A:Molecule type: DNA  
 A:Residues: 1-151 <ALB>  
 A:Cross-references: GB:X64346; NID:960320; PIDN:CAA5636.1; PID:960334  
 R:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.; W  
 J. Virol. 66, 5047-5058, 1992  
 A:Title: Primary structure of the herpesvirus saimiri genome.  
 A:Reference number: A37309; MUID:92333688; PMID:1321287  
 A:Contents: annotation; protein-coding frames  
 A:Note: neither protein nor nucleotide sequence is given  
 C:Genetics:  
 A:Gene: 13  
 C:Superfamily: saimiri herpesvirus immediate-early protein 2  
 C:Keywords: early protein

Query Match 9.5%; Score 93.5; DB 1; Length 151;  
 Best Local Similarity 23.0%; Pred. No. 0.17; 65; Indels 41; Gaps 8;  
 Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;  
 Oy 11 SLSLFLQVVAFLANWGTHTYSHWPCSCPGDSTSEELL-----RSTVPPPLLEPA 65  
 Db 6 TSLVLLLL--LSIDCIYKSEITSAQTPRCCLANNSPFRSVAVTLSTIRWNT----- 54  
 Oy 66 RPNRHPSCRASEDGPLNSRAISPMRYELDRDLNRLPDLVHARCLCPHCVSLOTGSHMD 125  
 Db 55 -----SSKRASD---YYNRSTSPMTLHRNEDODRPSVIEAKCRIGYGCYNAD----- 99  
 Oy 126 PRGNSSELYHNOGYFYRRPC---HGKGTGKGYCLERRLRVSLACVCPVPRV 175  
 Db 100 --GNVD--YHNSVPDQOELLVVRKHQPCPNFRLKML--VTVGCTCVTPIV 147

RESULT 3  
 149623  
 Cytoxic T-lymphocyte-associated antigen 8 precursor - mouse  
 N:Alternate names: immediate-early protein 2 (ORF13) homolog  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 26-Aug-1999  
 C:Accession: J49623  
 R:Rouvier, E.; Luciani, M.  
 J. Immunol. 150, 5445-5456, 1993  
 A:Title: CTLA-8, cloned from an activated T cell, bearing AU-rich messenger RNA instabl  
 A:Reference number: 149623; MUID:93294300; PMID:8390535  
 A:Accession: J49623  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-150 <RES>  
 A:Cross-references: GB:J13839; NID:9293329; PIDN:AAA37490.1; PID:9293330  
 C:Genetics:  
 A:Gene: Ctla8  
 C:Superfamily: saimiri herpesvirus immediate-early protein 2

Query Match 9.2%; Score 91; DB 2; Length 150;  
 Best Local Similarity 29.7%; Pred. No. 0.29; 44; Indels 10; Gaps 5;  
 Matches 30; Conservative 17; Mismatches 44; Indels 10; Gaps 5;  
 Oy 73 SCRASEDCPLN--SRAISPMRYELDRDLNRLPDLVHARCLCPHCVSLOTGSHMDPRGNS 130  
 Db 50 SSKASRRPSDYLNKSTSPMTLSRNEPDPRPSVIMEAQCRHQCVAE--GKLDHMHNS 107  
 Oy 131 ELVYHNOGVFYRRPCHEKGTGKGYCLERRLRVSLACVY 171  
 Db 108 VLIQOELLVLRKP---EKCPFT-FRVEKML--VGVCCTCV 142

RESULT 4  
 A60503

sperm-binding glycoprotein ZP3 precursor - golden hamster  
 N:Alternate names: sperm receptor; zona pellucida glycoprotein ZP3  
 C:Species: Mesocricetus auratus (golden hamster)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A60503  
 R:Kinsch, R.A.; Ruiz-Seller, B.; Wassarman, P.M.  
 Dev. Biol. 142, 414-441, 1990  
 A:Title: Genomic organization and polypeptide primary structure of zona pellucida 9  
 A:Reference number: A60503; MUID:91078540; PMID:2257975  
 A:Accession: A60503  
 A:Molecule type: DNA  
 A:Residues: 1-422 <KIN>  
 A:Cross-references: GB:M63629  
 A:Note: The authors translated the codon CAA for residue 251 as Glu, and AGC for re  
 C:Comment: This sulfated glycoprotein in the zona pellucida of the oocyte is a rece  
 C:Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology  
 C:Keywords: glycoprotein; oocyte  
 F:45-300/Domain: ZP domain homology <ZFP>

Query Match 9.0%; Score 88.5; DB 1; Length 422;  
 Best Local Similarity 28.8%; Pred. No. 1.4; 46; Indels 39; Gaps 9;  
 Matches 42; Conservative 19; Mismatches 46; Indels 39; Gaps 9;  
 Oy 7 LGEDS--SLISLFLQVVAFLANWGTHTYSHWPCSCPGDSTSEELLRMSTV-----P 58  
 Db 73 LGSENCRPLVSAVDVVFRAQL--HE-----CSNRQVT-EDALVSTVLLHQP RP 121  
 Oy 59 VPPLPAPNRH--PESCRASEDGPLNSRAISPMRYELDRDLN-----RLPDLX 107  
 Db 122 VPGSLIRTNADVPIDRYPGQNSSHAIRPTMVFPSTVSSEKLVFSLRLMEKNW 181  
 Oy 108 ARCLCP--HC-----VSLDTGSHM 124  
 Db 182 TEKLSPTSHLGEVAVYLAQVQTSHL 207

RESULT 5  
 JC4628  
 Cytoxic T-lymphocyte-associated antigen 8 precursor - mouse  
 N:Alternate names: CTLA8 protein  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 26-Aug-1999  
 C:Accession: JC4628  
 R:Xiao, Z.; Timour, M.; Painter, S.; Fanslow, W.; Spriggs, M.  
 Gene 168, 223-225, 1996  
 A:Title: Complete nucleotide sequence of the mouse CTLA8 gene.  
 A:Reference number: JC4628; MUID:96194901; PMID:8654948  
 A:Accession: JC4628  
 A:Molecule type: DNA  
 A:Residues: 1-147 <YAO>  
 A:Cross-references: GB:U35108; NID:91244499; PIDN:AAA93253.1; PID:91244500  
 C:Genetics:  
 A:Gene: ctla8  
 A:Introns: 69/2  
 C:Superfamily: saimiri herpesvirus immediate-early protein 2  
 C:Keywords: cytokine; glycoprotein; lymphocyte  
 F:1-14/Domain: signal sequence #status predicted <Sig>  
 F:15-147/product: cytoxic T-lymphocyte-associated antigen 8 #status predicted <MA  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.7%; Score 86; DB 2; Length 147;  
 Best Local Similarity 27.3%; Pred. No. 0.83; 40; Indels 8; Gaps 3;  
 Matches 24; Conservative 16; Mismatches 40; Indels 8; Gaps 3;  
 Oy 84 SRAISPMRYELDRDLNRLPDLVHARCLCPHCVSLOTGSHMDPRGNSSELYHNOGYFYRR 143  
 Db 60 NRSTSPMTLHRNEDPDPRPSVIMEAQCRHQCVAE--GKLDHMHNSVLIQOELLVLRKRE 117  
 Oy 144 PCHKEGTGKGYCLERRLRVSLACVY 171  
 Db 118 P-----ESCPFTFRVEKML--VGVCCTCV 139

	Query Match	8 4%:	Score 83:	DB 2:	Length 1323:	
	Best Local Similarity	26.7%:	Pred. No. 15:			
	Matches	35:	Conservative	7:	Mismatches	39:
					Indels	50:
					Gaps	7:
QY	54 WSTVPVPLEPBAR--PKNRHESCRASEDGP-----NSRAISPMRYELDRDLNRLRQ	103				
	:                               :					
Db	1202 WAAGR-PRRRARRCGSRPHNRPRASRARAAAHNNHRRAAGGWDP-PPRAPTSRSLE	1260				
QY	104 DL-----YHARCLSPHY-----SLDTGSHMDPGNSSELYHNQTGFYER	143				
Db	1261 DLSGCPRAAPTTRLTGPSRHAR-RGRNAANMGSPRLPTASHRNHRNG-----	1304				
QY	144 PCHGEKFTNGS	154				
	:       :					
Db	1305 ---GDLGTRRG	1312				

Query Match	8.3%	Score 81.5;	DB 2;	Length 46/;
Best Local Similarity	30.3%;	Pred. No. 7;		
Matches 33;	Conservative 8;	Mismatches 37;	Indels 31;	Gaps 5

	Query Match	8.0%	Score 78.5	Df 2	Length 206
	Best Local Similarity	20.0%	Pred. No. 5	8	
	Matches	33	Conservative	21	Mismatches 46; Gaps 65;
OY	34 SHMPSCPS-----RCGDTSELLLMVSVPRYLEPARNRHRCSRA-----S 77				
Db	63 SHSPSLAPSTQOALLRLQVKGKLNHGEDIITSS-----GKSNCKKKLDITIS 106				

A:Accession JQ0805  
A:Molecule type: DNA  
A:Residues: 1-358 <MEN>  
A:Cross-references: GB:M33152; NID:g142310; PIDN:AAA82505.1; PID:g142311  
A:Experimental source: strain OP  
A>Note: Part of this sequence, including the amino end of the mature protein, was  
C:Genetics:  
A:gene: hoxx  
C:domain: heterodimer; large and small chain  
C:Function:  
A:Pathway: hydrogen metabolism  
A:Note: contains iron-sulfur and nickel  
C:Superfamily: hydrogenase (Nfe) small chain  
C:Keywords: 3fe-4S; 4fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein  
F:1-45/Domain: signal sequence #status predicted <SIG>

F:46-358/Product: hydrotgenase small chain #status experimental <MAT>  
 F:62,65,160,199/Binding site: 4fe-4S cluster (Cys) (covalent) #status predicted  
 F:232,233,260,266/Binding site: 4fe-4S cluster (His, Cys, Cys) (covalent) (type N3)  
 F:275,294,297/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 7.9% Score 78; DB 1; Length 358;  
 Best Local Similarity 21.9%; Pred. No. 11;  
 Matches 37; Conservative 19; Mismatches 35; Indels 78; Gaps 11;

36 WPSCPSKQDTSSELLRWSTVPPLPPARPNRHPSCRASDGLNSRAISPMRYELD 95  
 DB 157 WSCSA-----SMGCV-----QAARPN-----PTQAVPIHKYITD 185  
 QY 96 RLNLRLPOLYLHARCLCPHCVSLQTS-----SHMDPRGNSLLY-----HNQTVF 140  
 DB 186 KPIYKVPV-----CPPIAEVMTGVITMFLFGKLPRLDRGPRPMFYGORIHDKC-- 235  
 QY 141 YRRPCH-----GKNGTHKGYCLERLYRVL-----ACVYR 172  
 DB 236 YRRP-HRDAGQFVHMDEGARRKGYC---LYKVGCKGPTSYNACSTVR 279

# RESULT 10

Thrombospondin 4 precursor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 06-Jan-1995 #sequence\_revision 11-Aug-1995 #text\_change 13-Aug-1999  
 C:Accession: A55710; S36069  
 R:Lawley, J.; McHenry, K.; Dugnette, M.; Derick, L.  
 J. Biol. Chem. 270, 2809-2814, 1995  
 A:Title: Characterization of human thrombospondin-4.  
 A:Reference number: A55710; MUID:95153552; PMID:7852353  
 A:Accession: A55710  
 A:Molecule type: mRNA  
 A:Residues: 1-961 <LW>  
 A:Cross-references: EMBL:Z19585; NID:9311625; PIDN:CAAT9635.1; PID:9311626  
 A:Note: authors translated the codon GTG for residue 616 as Ser  
 C:Genetics:  
 A:Gene: GDB:THBS4  
 A:Cross-references: GDB:463011; OMIM:600715  
 A:Map position: 1q21-1q23  
 C:Complex: homotrimer, disulfide linked  
 C:Function: participates in cell migration and adhesion, and in platelet aggregation  
 A:Description: thrombospondin 3; EGF homology  
 C:Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; cell ad  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-961/Product: thrombospondin 4 #status predicted <MAT>  
 F:290-324/Domain: EGF homology <EGF>  
 F:330-362/Domain: EGF homology <EGF>  
 F:562-564/Region: cell attachment (R-G-D) motif  
 F:503/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:343/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
 F:612,941/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.9% Score 77.5; DB 1; Length 961;  
 Best Local Similarity 27.3%; Pred. No. 34;  
 Matches 38; Conservative 13; Mismatches 47; Indels 41; Gaps 8;

QY 7 LGEDSLISLFLQVAVFLAMVMTHTYSHMPCPSKQDTSSELLRWSTV--PVPLLP 64  
 DB 234 LGVKKDLROQVETSF-----RMTIAEQACGPKLFQSPTP-----STVADAPAPAP 283  
 QY 65 ARPNRHHES-----CRASED-----GPLNSRAISPMRYE-----LDRNLRLPOLLY 106  
 DB 284 TRPRRDSNSPCFRGVQCTDSRDFQCGP-----CPGTYGNGITCIDVD-----ECKY 332  
 QY 107 HARCLCPHCVSLQTSQSHMD 125  
 DB 333 HPCYRGVHCINLSPEGRCD 351

# RESULT 11

148742  
 C:Species: Neurospora crassa  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 19-May-2000  
 C:Accession: T48742  
 R:Schulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyaka  
 submitted to the Protein Sequence Database, April 2000  
 A:Reference number: 224541  
 A:Accession: T48742  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-263 <SCA>  
 A:Cross-references: EMBL:AL353819; GSPDB:GN00112; NCSP:BD4.160  
 A:Experimental source: cosmid contig 8D4; strain 74

Query Match 7.8% Score 77; DB 2; Length 263;  
 Best Local Similarity 25.4%; Pred. No. 10;  
 Matches 34; Conservative 11; Mismatches 45; Indels 44; Gaps 8;

QY 36 WPSCPSKQDTSSE--ELRW--STVPVPLPPARPN-RHPSCRASE----- 78  
 DB 43 WSSSLPVEGKSKKATSRVGMASVEVPSAKARARLRTDHCRRPMTYLRDRDMEAG 102  
 QY 79 -----DGPL-----NSRAISPMRYE-----LDRNLRLPOLY-----YARCLCPH----- 114  
 DB 103 GSGRRPMDGFLPQCGRCHALYVWENSPSYDRSNANAOVLGALKRHRACPRQLSSL 162  
 QY 115 --CVSLQTSQSHMD 125  
 DB 163 DGLCVRCYTGRTD 176

# RESULT 12

111776  
 hydroxynase (EC 1.18.99.1) (uptake) small chain precursor - Azotobacter chroococcum  
 C:Species: Azotobacter chroococcum  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 20-Apr-2000  
 C:Accession: S11776  
 R:Forst, C.M.; Garg, N.; Garg, R.P.; Tidellius, K.H.; Yates, W.G.; Arp, D.J.; Seefeld  
 Mol. Microbiol. 4, 999-1008, 1990  
 A:Title: The identification, characterization, sequencing and mutagenesis of the ge  
 A:Reference number: S11776; MUID:91014699; PMID:2215219  
 A:Accession: S11776  
 A:Molecule type: DNA  
 A:Residues: 1-344 <FOR>  
 A:Cross-references: EMBL:X52961; NID:938713; PIDN:CAAT37133.1; PID:938714  
 A:Experimental source: strain MCD1  
 C:Genetics:  
 A:Gene: hups  
 C:Complex: heterodimer; large and small chain  
 C:Function:  
 A:Pathway: hydrogen metabolism  
 A:Note: contains iron-sulfur and nickel  
 C:Superfamily: hydrogenase (Nlfe) small chain  
 C:Keywords: 3fe-4S; 4fe-4S; heterodimer; hydrogen metabolism; iron-sulfur protein;  
 F:1-34/Domain: signal sequence #status predicted <SIG>  
 F:35-344/Product: hydrogenase (uptake) small chain #status predicted <MAT>  
 F:51,54,146,180/Binding site: 4fe-4S cluster (Cys) (covalent) #status predicted  
 F:218,221,246,252/Binding site: 4fe-4S cluster (His, Ser, Cys, Cys) (covalent) (tp  
 F:261,280,283/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 7.8% Score 77; DB 1; Length 344;  
 Best Local Similarity 21.3%; Pred. No. 13;  
 Matches 36; Conservative 21; Mismatches 34; Indels 78; Gaps 11;

QY 36 WPSCPSKQDTSSELLRWSTVPVPLPPARPNRHPSCRASEDGLNSRAISPMRYELD 95  
 DB 143 WSCSA-----SMGCV-----QAARPN-----PTQAVPIHKYITD 171

QY 96 RDNLRLPDLYHARCLCPHCVSLOTG-----SHMDRGNSELLY-----HNOTVE 140  
 DB 172 KPMIKVPG-----CPRIAEVMGVITMYLTFGLKPLDGRGKMYGGQRINRKS-- 221  
 QY 141 YRRPCH-----GEGTKHGYCLERLYRVSL-----ACVCVR 172  
 DB 222 YRRP-HEFDAGQFVEHMDDEGARKGYC-----LYKVGCKGPTSYNACSTVR 265

## RESULT 13

S27224  
 N-methyl-D-aspartate receptor epsilon-4 chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 25-Feb-1994 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-1999  
 C:Accession: S27224  
 R:Ikeda, K.; Nagasawa, M.; Mori, H.; Araki, K.; Sakimura, K.; Watanabe, M.; Inoue, Y.; M  
 FEBS Lett. 313, 34-38, 1992  
 A:Title: Cloning and expression of the epsilon-4 subunit of the NMDA receptor channel.  
 A:Reference number: S27224; MUID:93050214; PMID:1385220  
 A:Accession: S27224  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1323 <IKE>  
 A:Cross-references: EMBL:DJ2822  
 C:Superfamily: N-methyl-D-aspartate receptor 2D; glutamate receptor homology  
 C:Keywords: transmembrane protein  
 F:451-879/Domain: glutamate receptor homology <GRH>

Query Match 7.8%; Score 76.5; DB 2; Length 1323;  
 Best Local Similarity 25.5%; Pred. No. 59;  
 Matches 35; Conservative 6; Mismatches 41; Indels 55; Gaps 7;

QY 54 WSTVPV-----PLEPAR-----PNRNPESCRASEDGPL-----NSRAISPMRYELDRD 97  
 DB 1195 WAPRRPAAAPRRARRRRCGRPRNRPRASHRAAARNHNRRAAGGMDLPPRAP 1254  
 QY 98 LNRLEPDL-----YHARCLCPHCY-----SLDTGSHMDRGNSELLYHNO 137  
 DB 1255 TSSLEDLSSCPRAAPRTLRTPSRNAR-RCPNAAHMGCPRLTASHRRNRG----- 1304  
 QY 138 TVFYRRPCHGEKTHKG 154  
 DB 1305 -----GDLGTRRG 1312

## RESULT 14

G85064  
 hypothetical protein AT4G05150 (imported) - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
 C:Accession: G85064  
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
 Nature 402, 769-777, 1999  
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A:Reference number: A85001; MUID:20083488; PMID:10617198  
 A:Accession: G85064  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-446 <STO>  
 A:Cross-references: GB:NC\_001268; NID:97267274; PIDN:CAB81057.1; GSPDB:GN00140  
 C:Genetics:  
 A:Gene: AT4G05150  
 A:Map position: 4

Query Match 7.7%; Score 75.5; DB 2; Length 446;  
 Best Local Similarity 22.7%; Pred. No. 24;  
 Matches 30; Conservative 21; Mismatches 44; Indels 37; Gaps 6;

QY 44 GQDTSSELRNMTVPVPP-----LEPAR-----NRHPSCRASEDGPLNSRAISPMRY 92  
 DB 249 GSTSSAVVMRISTELPPPVPIKPSPEPVSTPKSNPQEQVMOOSNLPLVNSQ---WQY 304

QY 93 E-----LDRLNRLPDLYHARCLCPHCVSLOTGSHMDRGNSELL----- 132  
 DB 305 ARPGQOQVHYGGHTTHQSP--VYVPGSYRGNHNMVQGGHNMVQPGNMVQVMPQOYLQ 362  
 QY 133 LYHNOTVFYRRP 144  
 DB 363 QYHNVPMGYHQP 374

## RESULT 15

T14764  
 hypothetical protein DKFZp434H204.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T14764  
 R:Wambolt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, August 1999  
 A:Reference number: T18181  
 A:Accession: T14764  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-898 <NAN>  
 A:Cross-references: EMBL:AL110226  
 A:Experimental source: adult testis; clone DKFZp434H204  
 C:Genetics:  
 A:Note: DKFZp434H204.1

Query Match 7.7%; Score 75.5; DB 2; Length 898;  
 Best Local Similarity 24.4%; Pred. No. 49;  
 Matches 31; Conservative 9; Mismatches 48; Indels 39; Gaps 6;

QY 34 SHWPSCPSPGQDTSSELRNMTVPVPP--EPARNHNPESCRASEDGPLNSRAISPMR 91  
 DB 739 SSMRECSACGGGEQORLY--TCPEGLCEALRP-----TTRCNHPTQVWVGFW- 790  
 QY 92 YELDDLRNLPDLYHARCLCP-----HCVSLDTGSHMDRGNSELLYHNOTVY 141  
 DB 791 -----GQCSAPCGGQVQRRLYKCVNTOTGL--PEEDSDCGHNAWPS 831  
 QY 142 RRPCHGE 148  
 DB 832 SRPCGE 838

Search completed: February 26, 2003, 09:33:28  
 Job time : 49 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:08:55 ; Search time 13 Seconds  
(without alignments)  
564.716 Million cell updates/sec

Title: US-10-000-157-6

Perfect score: 985  
Sequence: 1 MRRPRPLGDSLSLFLVY.....ERRLYRVSLACVPRVPMG 177

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	985	100.0	177	117E_HUMAN	Q9H293 homo sapien
2	165.5	16.8	197	117C_HUMAN	Q9P0M4 homo sapien
3	125.5	12.7	180	117B_HUMAN	Q9H293 homo sapien
4	123.5	12.5	180	117F_MOUSE	Q9H293 mus musculu
5	122	12.4	153	117E_HUMAN	Q9H293 homo sapien
6	116.5	11.8	178	117B_MOUSE	Q9H293 mus musculu
7	105.5	10.7	153	117C_HUMAN	Q9H293 homo sapien
8	93.5	9.5	151	117D_HUMAN	Q9H293 mus musculu
9	91	9.2	150	117E_MOUSE	Q9H293 mus musculu
10	90.5	9.2	151	117F_MOUSE	Q9H293 mus musculu
11	88.5	9.0	151	117G_MOUSE	Q9H293 mus musculu
12	83	8.4	133	117H_MOUSE	Q9H293 mus musculu
13	81.5	8.3	133	117I_MOUSE	Q9H293 mus musculu
14	78	7.9	133	117J_MOUSE	Q9H293 mus musculu
15	77.5	7.9	133	117K_MOUSE	Q9H293 mus musculu
16	77.5	7.9	133	117L_MOUSE	Q9H293 mus musculu
17	77.5	7.9	133	117M_MOUSE	Q9H293 mus musculu
18	77.5	7.9	133	117N_MOUSE	Q9H293 mus musculu
19	77.5	7.9	133	117O_MOUSE	Q9H293 mus musculu
20	77.5	7.9	133	117P_MOUSE	Q9H293 mus musculu
21	76.5	7.8	133	117Q_MOUSE	Q9H293 mus musculu
22	76.5	7.8	133	117R_MOUSE	Q9H293 mus musculu
23	76.5	7.8	133	117S_MOUSE	Q9H293 mus musculu
24	76.5	7.8	133	117T_MOUSE	Q9H293 mus musculu
25	76.5	7.8	133	117U_MOUSE	Q9H293 mus musculu
26	76.5	7.8	133	117V_MOUSE	Q9H293 mus musculu
27	76.5	7.8	133	117W_MOUSE	Q9H293 mus musculu
28	76.5	7.8	133	117X_MOUSE	Q9H293 mus musculu
29	76.5	7.8	133	117Y_MOUSE	Q9H293 mus musculu
30	76.5	7.8	133	117Z_MOUSE	Q9H293 mus musculu
31	76.5	7.8	133	117A_MOUSE	Q9H293 mus musculu
32	76.5	7.8	133	117B_MOUSE	Q9H293 mus musculu
33	76.5	7.8	133	117C_MOUSE	Q9H293 mus musculu

34	72.5	7.4	1254	1	POL5_EEYVM	P36331 venezuelan
35	72.5	7.4	3695	1	LMA5_HUMAN	O15230 homo sapien
36	72.5	7.4	3744	1	YBP9_YEAST	P38811 saccharomyc
37	72.5	7.4	238	1	IBP6_MOUSE	P47880 mus musculu
38	72.5	7.3	391	1	P53_RABIT	O06194 mus musculu
39	71.5	7.3	2319	1	F8A2_MOUSE	P24347 mus musculu
40	71.5	7.2	488	1	FW11_HUMAN	O07889 homo sapien
41	71.5	7.2	1333	1	SOS1_HUMAN	O05014 manchester
42	71.5	7.2	2208	1	POLN_MANCV	P35419 mus musculu
43	70.5	7.2	914	1	PERT_MOUSE	P23507 xenopus lae
44	70.5	7.1	198	1	XAL1_XENLA	O824c5 salmoneilla
45	70	7.1	479	1	FLRD_SALTI	

## ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	177 AA.
AC	117E_HUMAN			
DF	15-JUN-2002 (Rel. 41, Created)			
DF	15-JUN-2002 (Rel. 41, Last sequence update)			
DF	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-17E precursor (IL-17E).			
GN	IL17E.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI-TaxID:9606;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-21125711; PubMed-11058597;			
RA	Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,			
RA	Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;			
RT	IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog			
RT	IL-17Rhl."			
RL	J. Biol. Chem. 276:1660-1664(2001).			
CC	-1- FUNCTION: Induces activation of NF-kappaB and stimulates			
CC	production of the proinflammatory chemokine IL-8;			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Expressed at low levels in several tissues,			
CC	including brain, kidney, lung, prostate, testis, spinal cord,			
CC	adrenal gland, and trachea.			
CC	-1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; AF305200; AAC0848.1;			
DR	Gene; HGNC:13765; IL17E.			
DR	MIM: 605658;			
KM	Cytokine; Glycoprotein; Signal.			
FT	CHAIN	1	32	POTENTIAL.
FT	DISULFID	33	177	INTERLEUKIN-17E.
FT	DISULFID	110	168	BY SIMILARITY.
FT	CARBOHYD	115	170	BY SIMILARITY.
FT	SEQUENCE	136	136	N-LINKED (GLCNAc). (POTENTIAL).
SO	SEQUENCE	177 AA;	20330 MW;	52D895710CD59871 CRC64;

Query Match 100.0%; Score 985; DB 1; Length 177;  
Best Local Similarity 100.0%; Pred. No. 1.7e-86;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 MRRPRPLGDSLSLFLVYVFLAVWVGTHRTYSHMPCCPKSGQDTSELLRWSTVPP 60
DB	1 MRRPRPLGDSLSLFLVYVFLAVWVGTHRTYSHMPCCPKSGQDTSELLRWSTVPP 60

OY 61 PLEPARPNHPSRCRASEGDLNRAISPMRYELDRNLRLPODLYHARCPCFHCYSLOT 120  
 DB 61 PLEPARPNHPSRCRASEGDLNRAISPMRYELDRNLRLPODLYHARCPCFHCYSLOT 120  
 OY 121 GSHMDRGNSSELLYHNOTVYFRRPCHGKGTAKGKCYCLERLYVSLACVCPRRWG 177  
 DB 121 GSHMDRGNSSELLYHNOTVYFRRPCHGKGTAKGKCYCLERLYVSLACVCPRRWG 177

RESULT 2  
 ID 117C\_HUMAN STANDARD: PRT: 197 AA.  
 AC 09P0M4: 09HC75:  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17C precursor (IL-17C) (Cytokine CX2).  
 GN IL17C.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20105548; PubMed-10639155;  
 RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,  
 RA Gunney A.L., Wood W.I.;  
 RA "Cloning and characterization of IL-17B and IL-17C, two new members  
 RT of the IL-17 cytokine family.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., He L., Wan T., Yuan Z., Cao X.;  
 RA "Novel human cytokine CX2 with homology to IL-17.";  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha  
 CC and IL-1beta from the monocytic cell line THP-1.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL: AF152099; AAF28105.1;  
 CC EMBL: AF142410; AAG27921.1;  
 CC Genew: HGNC:5983; IL17C.  
 DR MIM: 604628;  
 DR Cytokine; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 197 INTERLEUKIN-17C.  
 FT DISULFID 129 189 BY SIMILARITY.  
 FT DISULFID 134 191 BY SIMILARITY.  
 FT CONFLICT 30 50 H -> R (IN REF. 2).  
 FT SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;

Query Match 16.8%; Score 165.5; DB 1; Length 197;  
 Best Local Similarity 29.7%; Pred. NO. 8.8e-09;  
 Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;

OY 31 HTYSHMPSRCPKQDTSEEL-----LRM-STYP-----VPLEPARPNHPS 73  
 DB 27 HPHSHGPHPCYS-----AELPLQADPPHLLARAKAGQALPVALLVSLLEAASHRGRR 81  
 OY 74 CRASEDGPL-----NSRAISPMRYELDRNLRLPODLYHARCPCFHCYSLOTGS 122  
 DB 82 PSATTTQCIVLAPPEVLEADTHQHSISPMRYELDRNLRLPODLYHARCPCFHCYSLOTGS 141  
 OY 123 HMDPRGNSSELLYHNOTVYFRRPCHGKGTAKGKCYCLERLYVSLACVCPRR 174

DB 142 ETRAL-NSVRLLOSLLVLRRCRSGSLPFGARAFHTEFIHVPGCTCVLPR 195  
 ID 117B\_HUMAN STANDARD: PRT: 180 AA.  
 AC 09UHF5:  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17B precursor (IL-17B) (Cytokine-like protein ZCYT07)  
 DE (Neuronal Interleukin-17 related factor) (Interleukin-20).  
 GN IL17B OR ZCYT07 OR N1RF OR IL20.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,  
 RA Martinez T., Hoffman R., O'Hara P.;  
 RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20317118; PubMed-10749887;  
 RA Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,  
 RA Barber M.C., Wang W., Mathen K., Hodge V., Fisher C.L., Olsen H.,  
 RA Ruben S.M., Knayazov I., Cho Y.H., Kao V., Wilkinson K.A.,  
 RA Darrell J.A., Ehner R.;  
 RA "A novel cytokine receptor-ligand pair. Identification, molecular  
 RT characterization, and in vivo immunomodulatory activity.";  
 RT J. Biol. Chem. 275:19167-19176(2000).  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20105548; PubMed-10639155;  
 RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,  
 RA Gunney A.L., Wood W.I.;  
 RA "Cloning and characterization of IL-17B and IL-17C, two new members  
 RT of the IL-17 cytokine family.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).  
 RL [4]  
 RP SEQUENCE FROM N.A.  
 RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Ledgern E.,  
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;  
 RA "Identification of a novel IL-17 related factor: demonstration of  
 RT neuronal expression and evaluation as a candidate for the chromosome  
 RT 5q-linked form of Charcot-Marie-Tooth disease.";  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 RL [5]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., Wang J., Cao X.;  
 RA "Novel cytokine homology with Interleukin-17.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Garrington D.P., Chung M.-W., Lee K.L., Pei C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha  
 CC and IL-1beta from the monocytic cell line THP-1.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed in adult pancreas, small intestine,  
 CC stomach, spinal cord and testis. Less pronounced expression in  
 CC prostate, colon mucosal lining, and ovary.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>



or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).

CC EMBL: AF184969; AAF01318.1; -

DR EMBL: AF212311; AAF78775.1; -

DR EMBL: AF152098; AAF28104.1; -

DR EMBL: AF216727; AAG44136.1; -

DR EMBL: AF10385; AAG3637.1; -

DR EMBL: AF386077; AAK60336.1; -

DR Genew; HGNC:5982; IL17B.

DR MIM: 604627; -

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 20

FT CHAIN 21 180

FT DISULFID 121 176

FT DISULFID 126 178

FT CARBOHYD 75 75

FT SEQUENCE 180 AA; 20437 MW; F1B0C1446DB1A4 CRC64;

Query Match 12.7%; Score 125.5; DB 1; Length 180;

Best Local Similarity 33.3%; Pred. No. 4.9e-05;

Matches 30; Conservative 16; Mismatches 39; Indels 5; Gaps 3;

OY 83 NSRAISPMRYEIDRLNLPDLYHARCLCPHCYSLGTGSHMDPRGNSLLYHNOVTYR 142

DB 94 NKRSISPFGYSINHPSPRIADLPPEARCLGCVNFT--MOEDRSWVSVFQVYR 151

OY 143 RPCHGEKGTHTKCYLERLRY-VSLACVY 171

DB 152 RLCPPPPRT--GPCRORAVMETIAGCTCI 179

RESULT 4

117B\_MOUSE STANDARD; PRT; 180 AA.

ID 117B\_MOUSE

AC Q90XT6; Q99MT3; Q9CT14;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-17 precursor (IL-17B) (Cytokine-like protein ZCYT07)

DE (Neuronal Interleukin-17 related factor) (Cytokine CX1).

OS IL17B OR ZCYT07 OR NTRF.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

OX NCBI

RN [1]

RP SEQUENCE FROM N.A.

RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J., Martinez T., Hoffman R., O'Hara P.

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguern E., Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.

RT "Identification of a novel IL-17 related factor: demonstration of neuronal expression and evaluation as a candidate for the chromosome 5q-linked form of Charcot-Marie-Tooth disease."

RT 5q-linked form of Charcot-Marie-Tooth disease.

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA STRAIN-BALB/C; X;

RC Zhang W., Cao X.

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA STRAIN-C57BL/6J; TISSUE-Embryo;

RC MEDLINE=21085660; PubMed=11217851;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiba H.,

Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carinacci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P., Nordone P., Ring B., Ringbach M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshnaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuki S., Hayashizaki Y.

RA Hayashizaki Y.

RA \*Functional annotation of a full-length mouse cDNA collection.\*

RL Nature 409:685-690(2001).

RP SEQUENCE FROM N.A.

RA Strausberg R.

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha and IL-1beta from the monocytic cell line THP-1 (by similarity).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>).

CC or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).

CC EMBL: AF184970; AAF01319.1; -

DR EMBL: AF218726; AAG44135.1; -

DR EMBL: AF250308; AAK37427.1; -

DR EMBL: AK003506; BAB22826.1; -

DR EMBL: BC002271; AAH02271.1; -

DR MGD; MGI:1928397; IL17b

KW Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 22

FT CHAIN 23 180

FT DISULFID 121 176

FT DISULFID 126 178

FT CARBOHYD 75 75

FT CONFLICT 1 7

FT CONFLICT 33 33

FT CONFLICT 34 34

FT CONFLICT 65 65

FT CONFLICT 76 76

FT SEQUENCE 180 AA; 20309 MW; E26FAC72001997C5 CRC64;

Query Match 12.5%; Score 123.5; DB 1; Length 180;

Best Local Similarity 32.2%; Pred. No. 7.6e-05;

Matches 29; Conservative 17; Mismatches 39; Indels 5; Gaps 3;

OY 83 NSRAISPMRYEIDRLNLPDLYHARCLCPHCYSLGTGSHMDPRGNSLLYHNOVTYR 142

DB 94 NKRSISPFGYSINHPSPRIADLPPEARCLGCVNFT--MOEDRSWVSVFQVYR 151

OY 143 RPCHGEKGTHTKCYLERLRY-VSLACVY 171

DB 152 RLCPPPPRT--GPCRORAVMETIAGCTCI 179

RESULT 5

117F\_HUMAN STANDARD; PRT; 153 AA.

ID 117F\_HUMAN

AC Q96PD4; Q9NUE6; Q96P18;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-17 precursor (IL-17F) (Interleukin-24) (Cytokine ML-1).

OS Homo sapiens (Human).

ID	IL17_HUMAN	STANDARD:	PRT:	155 AA.
Db	8	SILGLAFLESEAAARKIKVGHITFFQKRESP	-----	-PYVGGSMKLDIGI 51
Oy	67	PNRRPESGRASEDDPRLNSRAISPMRYELDRDLRLPDOLYHARCPCRCVSLDTGSHMR	126	
Db	52	IN-----ENQVRSMSNIESRSTSPWNTVYTMDPNRPSEVVOACRRNLIGINA	-----	101
Oy	127	RGNSELLYHN-----QTFYFRRPCHGSKGNHKGCCERRLRYRSLACVCP	173	
Db	102	GKEDISMSVPIQOETLVARRK---HGGGSVSFQLEKVL--VTVGCTCTP	147	
RESULT 6				
IL17B_MESAU	STANDARD:	PRT:	178 AA.	
IL17B_MESAU	QPEGL6:			
DR	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-17B precursor (IL-17B) (Neutrophil Interleukin-17 related factor) (Fragment).			
GN	IL17B OR NTRF			
OC	Mesocricetus auratus (Golden hamster).			
OC	Makroryta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MOORE E.E., Presnell S., Garrigues V., Guilbot A., Leguern E.,			
RA	Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;			
RT	Identification of a novel IL-17 related factor: demonstration of			
RT	neutrophil expression and evaluation as a candidate for the chromosome			
RT	5q-linked form of Charcot-Marie-Tooth disease."			
RL	Submitted (DEC-1999) to the EMBL/Genbank/DBS databases			
CC	1- FUNCTION: Stimulates the release of tumor necrosis factor alpha			
CC	and IL-1beta from the monocytic cell line THP-1 (By similarity).			
CC	1- SUBCELLULAR LOCATION: cytosol.			
CC	1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.			
CC	1- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	EMBL; AF218725; AAC64134.1;			
KW	Cyclokin; Glycoprotein; Signal.			
FT	CHAIN 1 22			
FT	SIGNAL 1 22			
FT	INTERLEUKIN-17B.			
FT	CARBOHYD 75 >178			
FT	DISULFID 121 175			
FT	DISULFID 126 178			
FT	NON_TER 178 178			
FT	SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;			
Query Match				
Best Local Similarity 32.6%; Pred. No. 0.00034;				
Matches 29; Conservative 14; Mismatches 41; Indels 5; Gaps 3				
Oy	83	NSRAISPMRYELDRDLRLPDOLYHARCPCRCVSLDTGSHMRGNSELLYHNQTFYR	142	
Db	94	NKRSLSPMGVSIINHPSRIPADLPARCLCGCVNPT--MQEDRSNVSIPVESQVYVR	151	
Oy	143	RPCHGSKGTHKGVCLEERLYR-VSLACV	170	
Db	152	RLC--PPPRPGRPCRRHYMETIANGCIC	178	
RESULT 7				
IL17_HUMAN	STANDARD:	PRT:	155 AA.	
IL17_HUMAN				



AC 016552;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Interleukin-17 precursor (IL-17) (IL-17A) (Cytotoxic T lymphocyte-  
 associated antigen 8) (CTLA-8).  
 GN IL17 OR IL17A OR CTLA8.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96281911; PubMed-8676080;  
 RA Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Alt-Yahia S.,  
 RA Mat C., Plin J.-J., Garlone P., Garcia E., Saeland S., Blanchard D.,  
 RA Galliard C., Das Mahapatra B., Rouvier E., Golstein P., Banchereau J.,  
 RA Lebecque S.;  
 RT "T cell interleukin-17 induces stromal cells to produce  
 RT proinflammatory and hematopoietic cytokines.";  
 RL J. Exp. Med. 183:2593-2603(1996).  
 RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-T-cell;  
 RX MEDLINE-96094436; PubMed-7499628;  
 RA Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M.,  
 RA Spligs M.K., Armitage R.J.;  
 RT "Human IL-17: a novel cytokine derived from T cells.";  
 RL J. Immunol. 155:5483-5486(1995).  
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND  
 CC HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE  
 CC INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.  
 CC -1- PIM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC -1- DATABASE: NAME-RED Systems' cytokine mit-reviews: IL17;  
 CC WWW="http://www.indsystems.com/asp/g\_silebuilder.aspbodyId=211".  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: Z58820; CA91233.1;  
 DR EMBL; U32659; AAC50341.1;  
 DR GeneW; HGNC:5981; IL17.  
 DR MIM: 603149;  
 KM Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
 FT CHAIN 1 23 POTENTIAL.  
 FT SIGNAL 1 23 INTERLEUKIN-17.  
 FT DISULFID 24 155 BY SIMILARITY.  
 FT DISULFID 94 144 BY SIMILARITY.  
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 155 AA; 17504 MW; 2BCA9C82F488601 CRC64;  
 Query Match 10.7%; Score 105.5; DB 1; Length 155;  
 Best Local Similarity 27.1%; Pred. No. 0.0033;  
 Matches 45; Conservative 27; Mismatches 73; Indels 21; Gaps 8;  
 QY 11 SLSLSFLQVVAFLAMVNGTHTYSHWPCSCPSKQDTSBELRMSTVPPV-PLEPAPRNR 69  
 DB 6 TSLVSLLL-LTSLDAIVAGITIPRNPCCPNSEDKNFR-----TVVNLNHNRRNT 58  
 QY 70 HPESRASEDEGLNRSATSPMYRELDRLNRLPDLNARCLCPHCVSLSQTSCHMDPRGN 129  
 DB 59 NKR--RSSD---YNNRSTSPNMLHNRDEPERPYIWEAK--CRHLGICINADGNDYHNN 111  
 QY 130 SELVYHNOTVFFYRPPCHGEGKTHKGYCLERLLRYSLACVAPR 175

Db 112 SVPIQCEIIVLRREP-CPNSFLREKIL-VSVGCTCVPLV 151  
 RESULT 8  
 ID VGI3\_HSVSA STANDARD; PRT; 151 AA.  
 AC P24916;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Immediate early gene 13 protein precursor.  
 GN 13 OR KCLF2.  
 OS Herpesvirus saimiri (strain 11).  
 OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 OC NCBI\_TaxID=10383;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-90163221; PubMed-2154888;  
 RA Albrecht J.-C., Fleckenstein B.;  
 RT "Structural organization of the conserved gene block of Herpesvirus  
 RT saimiri coding for DNA polymerase, glycoprotein B, and major DNA  
 RT binding protein.";  
 RL Virology 174:533-542(1990).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92333688; PubMed-1321287;  
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Blesinger B.,  
 RA Newman C.W., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,  
 RA Honess R.W.;  
 RT "Primary structure of the herpesvirus saimiri genome.";  
 RL J. Virol. 66:5047-5058(1992).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91021021; PubMed-1699352;  
 RA Nicholas J., Smith E.P., Coles L., Honess R.;  
 RT "Gene expression in cells infected with gammaherpesvirus saimiri:  
 RT properties of transcripts from two immediate-early genes.";  
 RL Virology 179:189-200(1990).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: X64346; CA45636.1;  
 DR EMBL; M31122; AAA46169.1;  
 DR EMBL; M60286; AAA46156.1;  
 DR PIR: D36807; D36807.  
 DR PIR: B45351; B45351.  
 KM Cytokine; Early protein; Signal.  
 FT CHAIN 1 22 POTENTIAL.  
 FT SIGNAL 1 22 IMMEDIATE EARLY GENE 13 PROTEIN.  
 FT CHAIN 23 151 BY SIMILARITY.  
 FT DISULFID 90 140 BY SIMILARITY.  
 FT DISULFID 95 142 BY SIMILARITY.  
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 151 AA; 17180 MW; 53BEDDE4206C432 CRC64;  
 Query Match 9.5%; Score 93.5; DB 1; Length 151;  
 Best Local Similarity 23.0%; Pred. No. 0.044;  
 Matches 40; Conservative 28; Mismatches 65; Indels 41; Gaps 8;  
 QY 11 SLSLSFLQVVAFLAMVNGTHTYSHWPCSCPSKQDTSBEL- RSTVVPPLPRA 65  
 DB 6 TSLVSLLL--LTSDICVKSSEITSAOTPRCLANNSPFRSVMVLTSLRNNNT----- 54

OY 66 RRRNRHESCRASEDGPPLNRAISPMRYELDRDLNRLPOLLYHARCPCVSLQTSMD 125  
 DB 55 -----SSKRAD--YYNRSTSPWTLNRNEDPRYPVIMEAKCYLCCVAND----- 99  
 OY 126 PRGNSELHNOCTVFRPRC---HGEKGTGKCYCLERLYRVSACVCPRPV 175  
 DB 100 --GNVD--YHMSVPIQOELLYVRKGHCPCPNSEFLKML--VTVCCTCVTPV 147

## RESULT 9

IL17\_RAT STANDARD: PRT; 150 AA.  
 ID IL17\_RAT

AC 061453:  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).  
 GN IL17 OR CTLA8.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93294300; PubMed=8390535;  
 RA Rouvier E., Luciani M.F., Mattei M.-G., Denizot F., Golstein P.;  
 RT CTLA-8, cloned from an activated T cell, bearing an intracellular messenger RNA instability sequences, and homologous to a herpesvirus salivari gene.  
 RT J. Immunol. 150:5445-5456(1993).  
 RL [2]  
 RP ORGANISM IDENTIFICATION.  
 RX MEDLINE=96194901; PubMed=8654948;  
 RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.;  
 RT \*Complete nucleotide sequence of the mouse CTLA8 gene.\*  
 RL Gene 168:223-225(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. AND ORGANISM IDENTIFICATION.  
 RX MEDLINE=97031826; PubMed=8877732;  
 RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A.,  
 RT Wagner J.L., Hannum C.H., Zlotnik A.;  
 RT \*House IL-17, a cytokine preferentially expressed by alpha beta TCR + CD4-CD8-T cells.\*  
 RL J. Interferon Cytokine Res. 16:611-617(1996).  
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE FROM MOUSE BUT, ON THE BASIS OF SUBSEQUENT WORK (REF.2 AND REF.3), HAS BEEN SHOWN TO BE OF RAT ORIGIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: L13839; AAA37490.1;  
 KM Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 150  
 FT DISULFID 89 139  
 FT DISULFID 94 141  
 FT CARBOHYD 63 63  
 FT CONFLICT 46 46  
 SQ SEQUENCE 150 AA: 16876 MW: 15333EDFD9D689F CRC64;

Query Match 9.2%; Score 91; DB 1; Length 150;  
 Best Local Similarity 29.7%; Pred. No. 0.075;  
 Matches 30; Conservative 17; Mismatches 44; Indels 10; Gaps 5;  
 OY 73 SCRASEDGPPLN--SRAISPMRYELDRDLNRLPOLLYHARCPCVSLQTSMDRGRS 130  
 DB 50 SSKASSRRSPDYLNRSTSPWTLNRNEDPRYPVIMEACRHRQCVNAE--GKLDHMS 107  
 OY 131 ELYHNOCTVFRPRC---HGEKGTGKCYCLERLYRVSACVCPV 171  
 DB 108 VLIQOELLYVRKGHCPCPNSEFLKML--VTVCCTCVTPV 142

## RESULT 10

IL17\_MOUSE STANDARD: PRT; 158 AA.  
 ID IL17\_MOUSE

AC 062386; Q60971;  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).  
 GN IL17 OR CTLA8.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=BA1B/C; TISSUE=Thymocytes;  
 RX MEDLINE=97031826; PubMed=8877732;  
 RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A.,  
 RT Wagner J.L., Hannum C.H., Zlotnik A.;  
 RT \*House IL-17, a cytokine preferentially expressed by alpha beta TCR + CD4-CD8-T cells.\*  
 RL J. Interferon Cytokine Res. 16:611-617(1996).  
 RL [2]  
 RP SEQUENCE OF 12-158 FROM N.A.  
 RX STRAIN=129/SV; TISSUE=T-cell;  
 RX MEDLINE=96194901; PubMed=8654948;  
 RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.;  
 RT \*Complete nucleotide sequence of the mouse CTLA8 gene.\*  
 RL Gene 168:223-225(1996).  
 CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES (BY SIMILARITY).  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: U43088; AAB05232.1;  
 DR EMBL: U3108; AAA3253.1;  
 DR GMD: MG1:107364; 1117;  
 KM Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
 FT SIGNAL 1 25  
 FT CHAIN 26 158  
 FT DISULFID 97 147  
 FT DISULFID 102 149  
 FT CARBOHYD 71 71  
 SQ SEQUENCE 158 AA: 17490 MW: 3505C143435F4653 CRC64;

Query Match 9.2%; Score 91; DB 1; Length 158;  
 Best Local Similarity 23.5%; Pred. No. 0.079;  
 Matches 39; Conservative 29; Mismatches 72; Indels 26; Gaps 7;

OY 11 SSLISLFLQVAVFLAMVGTHTYSHMPCSCPSKSG-----ODTSEELLKMWSTVVPPLPEPA 65  
 DB 6 ASSSVLMLLLSLAATVKAALIPSSACNTPEAKDPLQVKNVKNFNSIGA-KVSSR 64  
 OY 66 RPNRHPSCRASEDGPLNSRAISPWRELDRLRLODLYHACLCPCHCVSLOTGSHMD 125  
 DB 65 RPSDY-----LN-RSTSPWTLHRNEDPRYPVILAEACRORCVNAE--GKLD 110  
 OY 126 PRGSELLHNQTVFYRPRCHGEGKTHKCYCLERLYVSLACYV 171  
 DB 111 HHMSVLIQOELVLKREP-----ESCPFTFVEKML-VGVGCTCV 150

RESULT 11  
 VG13\_HSVSC STANDARD: PRT: 151 AA.

AC 040633: HSVSC  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Immediate early gene 13 protein precursor.  
 GN 13.  
 OS Herpesvirus saimiri (subgroup C / strain 488).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gammaherpesvirinae; Rhadinovirus.  
 OX NCBI\_TaxID=10384;  
 RN [1]  
 RP MEDLINE=98037620; PubMed=9371569;  
 RA Knape A., Hiler C., Thurnau H., Wiltmann S., Hofmann H.,  
 RA Fleckenstein B., Fleckenstein H.,  
 RT "The superantigen-homologous viral immediate-early gene iel4/vsag 1a  
 RT herpesvirus saimiri-transformed human T cells."  
 RL J. Virol. 71:9124-9133(1997).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: Y13183; CAA73627.1;  
 KM Cytokine; Early protein; Signal.  
 FT SIGNAL 1 22;  
 FT CHAIN 23 151 IMMEDIATE EARLY GENE 13 PROTEIN.  
 FT DISULFID 90 140 BY SIMILARITY.  
 FT DISULFID 95 142 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 9.2%; Score 90.5; DB 1; Length 151;  
 Best Local Similarity 23.0%; Pred. No. 0.084;  
 Matches 40; Conservative 27; Mismatches 66; Indels 41; Gaps 8;

OY 11 SSLISLFLQVAVFLAMVGTHTYSHMPCSCPSKSGODTSEELL-----RMSVVPPLPEPA 65  
 DB 6 TSVLULLL--LSIDCIYSEITSQTPRLAANNSFPSSVVTLSIRMNT----- 54  
 OY 66 RPNRHPSCRASEDGPLNSRAISPWRELDRLRLODLYHACLCPCHCVSLOTGSHMD 125  
 DB 55 -----SSKRASD--YVNRSTSPWTLHRNEDPRYPVILAEACRORCVNAE----- 99  
 OY 126 PRGSELLHNQTVFYRPRCHGEGKTHKCYCLERLYVSLACYVCPRPV 175  
 DB 100 --GNVD--YHNSVPIQOELLVVRKGHNPCPNSFRLEKML--VTVGCTCVPTIV 147

RESULT 12  
 ZP3\_MESAU STANDARD: PRT: 422 AA.  
 AC ZP3\_MESAU  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE zona pellucida sperm-binding protein 3 precursor (zona pellucida  
 DE glycoprotein zp3) (sperm receptor) (zona pellucida protein C).  
 GN zp3.  
 OS Mesocricetus auratus (golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP MEDLINE=91078540; PubMed=2257975;  
 RA Kinsch R.A., Ruiz-Seller B., Massarman P.M.;  
 RA "Genomic organization and polypeptide primary structure of zona  
 RA pellucida glycoprotein hzp3, the hamster sperm receptor."  
 RL Dev. Biol. 142:414-421(1990).  
 CC -1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR  
 CC SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE  
 CC SPECIES-SPECIFICITY OF THE INSEMINATION.  
 CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN  
 CC WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Extracellular  
 CC matrix.  
 CC -1- TISSUE SPECIFICITY: OOCYTES.  
 CC -1- DEVELOPMENTAL STAGE: GROWING OOCYTES.  
 CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.  
 CC -1- SIMILARITY: CONTAINS 1 ZP DOMAIN.

CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M63629; AAA37079.1;  
 DR InterPro: IPR001507; Endoglin/CD105.  
 DR Pfam: PF00100; zona\_pellucida: 1.  
 DR PRINTS: PRO0023; ZPPELLUCIDA.  
 DR SMART: SM00241; ZP: 1.  
 DR PROSITE: PS00682; ZP\_DOMAIN: 1.  
 KM Glycoprotein; Signal; Sulfation; Sperm; Receptor; Transmembrane;  
 FT SIGNAL 1 22  
 FT CHAIN 23 422  
 FT DOMAIN 23 386 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3.  
 FT TRANSMEM 387 407 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 408 422 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 45 306 ZP.  
 FT DOMAIN 119 158 PRO-RICH.  
 FT DOMAIN 208 257 PRO-RICH.  
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT SEQUENCE 422 AA; 45827 MW; D0F95BE7FF8E7E01 CRC64;

Query Match 9.0%; Score 88.5; DB 1; Length 422;  
 Best Local Similarity 28.8%; Pred. No. 0.4;  
 Matches 42; Conservative 19; Mismatches 46; Indels 39; Gaps 9;

OY 7 LGEDS--SLISLFLQVAVFLAMVGTHTYSHMPCSCPSKSGODTSEELLKMWSTV-----P 58  
 DB 73 LGSNCRPLVAVATDVVRKAQL--HE-----CSNRYQT-EDALVYSTVLLHQRP 121  
 OY 59 VPPLPAPNRH--PESCRASEDGPLNSRAISPWRELDRLN-----RLPODLVH 107



GN MAP3K8 OR TPL2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Long Evans; TISSUE-Liver;  
 RX MEDLINE=93211939; PubMed=7681591;  
 RA Patriotic C., Makris A., Bear S.E., Tsichlis P.N.;  
 RT "Tumor progression locus 2 (Tpl-2) encodes a protein kinase involved  
 in the progression of rodent T-cell lymphomas and in T-cell  
 activation.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2251-2255(1993).  
 RN (2)  
 RP FUNCTION, AND MAP3K8-NFKB1/P105 BINDING.  
 RX MEDLINE=99133929; PubMed=9950430;  
 RA Belich M.P., Salmeron A., Johnston L.H., Ley S.C.;  
 RT "P105, a kinase regulates the proteolysis of the NF-kappaB-inhibitory  
 protein NF-kappaB1 p105.";  
 RL Nature 397:363-368(1999).  
 CC -1- FUNCTION: Able to activate NF-kappa-B 1 by stimulating proteasome-  
 mediated proteolysis of NF-kappa-B 1/p105. Plays a role in the  
 cell cycle.  
 CC -1- SUBUNIT: Interacts with NFKB1/p105.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Expressed in spleen, thymus, liver and lung.  
 CC -1- PTM: Autophosphorylated.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC MAP KINASE KINASE KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; M94454; AAA42185.1; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRODOM: P000001; Euk\_pkinase.1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase: Serine/threonine-protein kinase; Proto-oncogene;  
 KW ATP-binding; Phosphorylation.  
 KW DOMAIN 146 388 PROTEIN KINASE.  
 FT NP\_BIND 144 152 ATP (BY SIMILARITY).  
 FT BINDING 167 167 ATP (BY SIMILARITY).  
 FT ACT\_SITE 253 253 BY SIMILARITY.  
 FT SEQUENCE 467 AA; 52807 MW; 454E0E32768A4ABD CRC64;  
 SQ  
 Query Match 8.3%; Score 81.5; DB 1; Length 467;  
 Best Local Similarity 30.3%; Pred. No. 2.1;  
 Matches 33; Conservative 8; Mismatches 37; Indels 31; Gaps 5;  
 OY 40 CPKSGQ--DTSEELRMSTVPPLEPAR-----PKRHPESCRASDGP 81  
 DB 50 CPSPNCKHSESLR-SGGEVPMLSVRYGTEDLLAFANHISNTTKHFRCPQSSGI 108  
 OY 82 LNSRAISP--WRYELDRDLNRLPQDLYHARCLCPHCVSLSGTGSHMDPRG 128  
 DB 109 LLMNVISPONGRYQIDSDVLLVPMKLTYYR-----SIGSGFVRG 147  
 RESULT 15  
 MBHS\_AZOV STANDARD; PRT; 358 AA.  
 ID MBHS\_AZOV  
 AC P21950;  
 DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Uptake hydrogenase small subunit precursor (EC 1.18.99.1)  
 DE (hydrogenlyase) (membrane-bound hydrogenase small subunit)  
 DE (hydrogenase beta subunit).  
 GN HOXK.  
 OS Acetobacter vinelandii.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Acetobacter  
 OX NCBI\_TaxID=354;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-UW;  
 RX MEDLINE=91092503; PubMed=2265761;  
 RA Menon A.L., Stults L.W., Robson R.L., Mortenson L.E.;  
 RT "Cloning, sequencing and characterization of the [NifE]hydrogenase-  
 encoding structural genes (hoxk and hoxg) from Acetobacter  
 vinelandii.";  
 RL Gene 96:67-74(1990).  
 CC -1- FUNCTION: THIS ENZYME RECYCLES THE H(2) PRODUCED BY NITROGENASE TO  
 INCREASE THE PRODUCTION OF ATP AND TO PROTECT NITROGENASE AGAINST  
 INHIBITION OR DAMAGE BY O(2) UNDER CARBON- OR PHOSPHATE-LIMITED  
 CONDITIONS.  
 CC -1- CATALYTIC ACTIVITY: 2 reduced ferredoxin + 2 H(+) = 2 oxidized  
 ferredoxin + H(2).  
 CC -1- COFACTOR: CONTAINS NICKEL AND IRON-SULFUR.  
 CC -1- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL SUBUNIT.  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.  
 CC -1- SIMILARITY: TO OTHER UPTAKE HYDROGENASES SMALL SUBUNIT.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL; M33152; AAA82505.1; -  
 DR EMBL; L23970; AAA19498.1; -  
 DR PIR: J00805; J00805.  
 DR HSSP: P12943; 1FRV.  
 DR InterPro: IPR002096; Cmp1x1\_20kDa.  
 DR InterPro: IPR001821; Nifhydrog\_small.  
 DR Pfam: PF01058; oxidored\_46; 1.  
 DR PRINTS: PR00614; NIFGNASESMIL.  
 DR TIGRFAMS: TIGR00391; hysda; 1.  
 KW Oxidoreductase; Signal; Membrane; Iron-sulfur; Nickel.  
 FT SIGNAL 1 45  
 FT CHAIN 46 358 UPTAKE HYDROGENASE SMALL SUBUNIT.  
 FT SEQUENCE 358 AA; 39259 MW; BDCE5646DA1D1C23 CRC64;  
 SQ  
 Query Match 7.9%; Score 78; DB 1; Length 358;  
 Best Local Similarity 21.9%; Pred. No. 3.3;  
 Matches 37; Conservative 19; Mismatches 35; Indels 78; Gaps 11;  
 OY 36 WPSCPSKGDSTSEELRMSTVPPLEPARPNHPSCRASEDGPLNSRAISFWYELD 95  
 DB 157 WGSQA-----SMWCV-----QAARPN-----PLQAVPIHKXYTD 185  
 OY 96 RDLNRLPQDLYHARCLCPHCVSLSGTG-----SHMDPRGNSSELY---HNOTVF 140  
 DB 186 KPIYKVG-----CPPIAEVMTGVTYTLGKPLPDLDRGQPKFYGORIHDKC-- 235  
 OY 141 YRRPCH-----GEKTHKGYCERLYRSL-----ACVGR 172  
 DB 236 YRRP-HPDAGQFVEMWDEGARKGYC---LYKVGCKGPTSYNACSTYR 279

Search completed: February 26, 2003, 09:31:57  
 Job time : 15 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2003, 09:26:55 ; Search time 31 Seconds  
(without alignments)  
1176.463 Million cell updates/sec

Title: US-10-000-157-6  
Perfect score: 985  
Sequence: 1 MRRPRRGGESSLSLFLQV.....ERRLYRVSLACVCVPRVWG 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_21.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_munc.\*  
9: sp\_organelle.\*  
10: sp\_phage.\*  
11: sp\_plant.\*  
12: sp\_rodent.\*  
13: sp\_virus.\*  
14: sp Vertebrate.\*  
15: sp\_unclassified.\*  
16: sp\_virus.\*  
17: sp\_bacteriopl.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	892	90.6	161	4	Q8WXB0
2	697	70.8	169	11	Q8VH88
3	652	66.2	153	11	Q8VHC9
4	126.5	12.8	202	4	Q8TAD2
5	114	11.6	111	11	Q8EAD7
6	107	10.9	162	5	Q44146
7	95	9.6	141	6	Q95156
8	87	8.8	499	5	Q9G234
9	83	8.4	405	4	Q9B021
10	83	8.4	547	10	Q9M5E9
11	81	8.2	1394	5	Q9V589
12	80.5	8.2	379	13	Q9NK28
13	80	8.1	358	1	Q9P914
14	79	8.0	862	11	Q9JIK1
15	78.5	8.0	174	10	Q8RVH7
16	78.5	8.0	206	5	Q22687

17	78	7.9	459	11	Q9DC55	Q9dC55 mus musculu
18	78	7.9	459	11	Q9D624	Q9d624 mus musculu
19	78	7.9	459	11	Q9CX88	Q9cX88 mus musculu
20	78	7.9	1090	10	Q8S1E5	Q8s1e5 oryza sativ
21	77	7.8	446	12	Q8ORP1	Q8orP1 chimpanzee
22	76.5	7.8	1615	11	Q9JMR4	Q9jM4 ratius norv
23	76	7.7	2434	10	Q94JB3	Q94JB3 oryza sativ
24	75.5	7.7	272	12	Q36279	Q36279 venezuelan
25	75.5	7.7	272	12	Q36281	Q36281 venezuelan
26	75.5	7.7	289	12	Q9QAR3	Q9qAR3 venezuelan
27	75.5	7.7	289	12	Q9QAR2	Q9qAR2 venezuelan
28	75.5	7.7	289	12	Q9QAR1	Q9qAR1 venezuelan
29	75.5	7.7	289	12	Q9QAR0	Q9qAR0 venezuelan
30	75.5	7.7	289	12	Q9QAS9	Q9qAS9 venezuelan
31	75.5	7.7	289	12	Q9QAS8	Q9qAS8 venezuelan
32	75.5	7.7	289	12	Q9QAS7	Q9qAS7 venezuelan
33	75.5	7.7	289	12	Q9QAS6	Q9qAS6 venezuelan
34	75.5	7.7	289	12	Q9QAS5	Q9qAS5 venezuelan
35	75.5	7.7	289	12	Q9QAS4	Q9qAS4 venezuelan
36	75.5	7.7	289	12	Q9YJL1	Q9yJL1 venezuelan
37	75.5	7.7	289	12	Q9W9J3	Q9w9J3 venezuelan
38	75.5	7.7	334	5	Q961F6	Q961F6 dirosophila
39	75.5	7.7	369	5	Q8SUP9	Q8sup9 encephalito
40	75.5	7.7	432	4	Q9NPM2	Q9nPM2 homo sapien
41	75.5	7.7	446	10	Q9M0X0	Q9m0X0 arabidopsis
42	75.5	7.7	477	10	Q94ON7	Q94ON7 arabidopsis
43	75.5	7.7	867	11	Q9JLF9	Q9jLF9 mus musculu
44	75.5	7.7	874	5	Q9VSE3	Q9vSE3 dirosophila
45	75.5	7.7	883	5	Q8SX53	Q8sX53 dirosophila

## ALIGNMENTS

RESULT 1	ID	Q8WXB0	PRELIMINARY:	PRT:	161 AA.
AC	Q8WXB0				
DT	01-MAR-2002 (TREMBlrel. 20, Created)				
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)				
DT	01-MAR-2002 (TREMBlrel. 20, Last annotation update)				
DE	1125.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID:9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-21629216; PubMed-11754819;				
RA	Fort M.W., Cheung J., Yen D., Li J., Zurawski S.M., Lo S., Menon S.,				
RA	Clifford T., Hunte B., Lesley R., Muchamuel T., Hurst S.D.,				
RA	Zurawski G., Leach M.W., Gorman D.M., Kennick D.M.;				
RT	"IL-25 Induces IL-4, IL-5, and IL-13 and Th2-Associated Pathologies In				
RT	Vivo.";				
RL	Immunity 15:985-995(2001).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Hurst S.D., Muchamuel T., Gorman D.M., Gilbert J.M., Clifford T.,				
RA	Kwan S., Menon S., Seymour B., Jackson C., Kung T., Bieleand J.,				
RA	Zurawski S.M., Chapman R., Zurawski G., Coffman R.L.;				
RT	"New IL-17 family members promote Th1 or Th2 responses in the lung: In				
RT	vivo function of the novel cytokine IL-25.";				
RL	Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.				
DR	EMBL, AF458059; AAL57622.1; - 32C85913PFEI51D CRC64;				
SO	SEQUENCE 161 AA; 18537 MW; 32C85913PFEI51D CRC64;				
QY	Query Match				
Db	Best local similarity 90.6%; Score 892; DB 4; Length 161;				
	Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
	19 QVAFPLAMWGRITTYSHWSPCCSCGODPSEELRMSTVVPPLPAPRRHRESCRAE 78				
	3 QVAFPLAMWGRITTYSHWSPCCSCGODPSEELRMSTVVPPLPAPRRHRESCRAE 62				





Query Match	Best Local Similarity	Score	DB 5	Length	DB 6	Length	DB 7	Length	DB 8	Length	DB 9	Length	DB 10	Length	DB 11	Length	DB 12	Length	DB 13	Length	DB 14	Length	DB 15	Length	DB 16	Length	DB 17	Length	DB 18	Length	DB 19	Length	DB 20	Length	DB 21	Length	DB 22	Length	DB 23	Length	DB 24	Length	DB 25	Length	DB 26	Length	DB 27	Length	DB 28	Length	DB 29	Length	DB 30	Length	DB 31	Length	DB 32	Length	DB 33	Length	DB 34	Length	DB 35	Length	DB 36	Length	DB 37	Length	DB 38	Length	DB 39	Length	DB 40	Length	DB 41	Length	DB 42	Length	DB 43	Length	DB 44	Length	DB 45	Length	DB 46	Length	DB 47	Length	DB 48	Length	DB 49	Length	DB 50	Length	DB 51	Length	DB 52	Length	DB 53	Length	DB 54	Length	DB 55	Length	DB 56	Length	DB 57	Length	DB 58	Length	DB 59	Length	DB 60	Length	DB 61	Length	DB 62	Length	DB 63	Length	DB 64	Length	DB 65	Length	DB 66	Length	DB 67	Length	DB 68	Length	DB 69	Length	DB 70	Length	DB 71	Length	DB 72	Length	DB 73	Length	DB 74	Length	DB 75	Length	DB 76	Length	DB 77	Length	DB 78	Length	DB 79	Length	DB 80	Length	DB 81	Length	DB 82	Length	DB 83	Length	DB 84	Length	DB 85	Length	DB 86	Length	DB 87	Length	DB 88	Length	DB 89	Length	DB 90	Length	DB 91	Length	DB 92	Length	DB 93	Length	DB 94	Length	DB 95	Length	DB 96	Length	DB 97	Length	DB 98	Length	DB 99	Length	DB 100	Length	DB 101	Length	DB 102	Length	DB 103	Length	DB 104	Length	DB 105	Length	DB 106	Length	DB 107	Length	DB 108	Length	DB 109	Length	DB 110	Length	DB 111	Length	DB 112	Length	DB 113	Length	DB 114	Length	DB 115	Length	DB 116	Length	DB 117	Length	DB 118	Length	DB 119	Length	DB 120	Length	DB 121	Length	DB 122	Length	DB 123	Length	DB 124	Length	DB 125	Length	DB 126	Length	DB 127	Length	DB 128	Length	DB 129	Length	DB 130	Length	DB 131	Length	DB 132	Length	DB 133	Length	DB 134	Length	DB 135	Length	DB 136	Length	DB 137	Length	DB 138	Length	DB 139	Length	DB 140	Length	DB 141	Length	DB 142	Length	DB 143	Length	DB 144	Length	DB 145	Length	DB 146	Length	DB 147	Length	DB 148	Length	DB 149	Length	DB 150	Length	DB 151	Length	DB 152	Length	DB 153	Length	DB 154	Length	DB 155	Length	DB 156	Length	DB 157	Length	DB 158	Length	DB 159	Length	DB 160	Length	DB 161	Length	DB 162	Length	DB 163	Length	DB 164	Length	DB 165	Length	DB 166	Length	DB 167	Length	DB 168	Length	DB 169	Length	DB 170	Length	DB 171	Length	DB 172	Length	DB 173	Length	DB 174	Length	DB 175	Length	DB 176	Length	DB 177	Length	DB 178	Length	DB 179	Length	DB 180	Length	DB 181	Length	DB 182	Length	DB 183	Length	DB 184	Length	DB 185	Length	DB 186	Length	DB 187	Length	DB 188	Length	DB 189	Length	DB 190	Length	DB 191	Length	DB 192	Length	DB 193	Length	DB 194	Length	DB 195	Length	DB 196	Length	DB 197	Length	DB 198	Length	DB 199	Length	DB 200	Length	DB 201	Length	DB 202	Length	DB 203	Length	DB 204	Length	DB 205	Length	DB 206	Length	DB 207	Length	DB 208	Length	DB 209	Length	DB 210	Length	DB 211	Length	DB 212	Length	DB 213	Length	DB 214	Length	DB 215	Length	DB 216	Length	DB 217	Length	DB 218	Length	DB 219	Length	DB 220	Length	DB 221	Length	DB 222	Length	DB 223	Length	DB 224	Length	DB 225	Length	DB 226	Length	DB 227	Length	DB 228	Length	DB 229	Length	DB 230	Length	DB 231	Length	DB 232	Length	DB 233	Length	DB 234	Length	DB 235	Length
-------------	-----------------------	-------	------	--------	------	--------	------	--------	------	--------	------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	-------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------



DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE Hypothetical 55.5 kDa protein.  
 OS Trypanosoma cruzi.  
 CC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 NCBI\_Taxid=5693;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Andersson B.  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF242860; AAF98145.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 499 AA; 55486 MW; 6727C831B8425296 CRC64;

Query Match 8.8%; Score 87; DB 5; Length 499;  
 Best Local Similarity 28.3%; Pred. No. 0.56;  
 Matches 32; Conservative 14; Mismatches 33; Indels 34; Gaps 6;

QY 37 PSCCPKGGDT---SEELRMSTVPVPLEPAPRNHPESCR-----ASEDGPLN-----83  
 DB 234 PSSPSDGFTRSMQQLIRKQSIPIPARHGE-KREPTDRQHLGSETERLNSGRHP 292  
 DB 293 SOOSSRVLS-----SPSNDVFHD-----TPIQSLHSGRRGYSI 329

## RESULT 9

ID Q9BU21 PRELIMINARY; PRT: 405 AA.  
 AC Q9BU21;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 19, Last annotation update)  
 DE Similar to hypothetical protein FLJ10101.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Straussberg R.  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC002945; AAH02945.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 405 AA; 44298 MW; 6C30D7F7B60DBE68 CRC64;

Query Match 8.4%; Score 83; DB 4; Length 405;  
 Best Local Similarity 24.3%; Pred. No. 1.2;  
 Matches 44; Conservative 10; Mismatches 51; Indels 76; Gaps 9;

QY 55 STVEVPLEPAPRNHPESCRASEDGPLNSRAI-----SPMYELDRDLRLPQ-----103  
 DB 217 SVPPVPEPSE-ALP---PAPCPSA---PAPRSIISRPPEGMRLGALGRGQMPWGGG 269  
 QY 104 -----DLNARCCP-----113  
 DB 270 RACHCLGRHLPLRYRLKCPAAVACASLELENGHWSFGMALQVGLQACEPALQEGRG 329  
 QY 114 HCVSIQTGSHNDPRGNSELLYHNTQVYRRPCHGKGTGKCYCLERRLYRVLACVYRP 173  
 DB 330 QLASARLGGHPPLG-----AEPVFLRDVTEAQEGPVR-VCLD-RLGRGLAVGALP 381

QY 174 R 174  
 DB 382 R 382

RESULT 10  
 ID Q9ME69 PRELIMINARY; PRT: 547 AA.  
 AC Q9ME69;

DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE rRNA -glycosidase (EC 3.2.2.22).  
 GN AAB.  
 OS Abrus precatorius (Indian joricoe) (Grab's eye).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eufrosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.  
 NCBI\_Taxid=3816;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-20102702; PubMed-10636890;  
 RX Liu C.L., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,  
 Lin J.Y.,

RT "Primary structure and function analysis of the Abrus precatorius  
 RT Agglutinin A chain by site-directed mutagenesis: Pro199 of Amphiphilic  
 RT alpha-Helix H Impairs Protein Synthesis Inhibitory Activity."  
 RL J. Biol. Chem. 275:1897-1901(2000).  
 CC - CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE  
 CC - SPECIFIC ADENOSINE ON THE 28S RNA.  
 CC - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING FAMILY.  
 CC EMBL: AF190173; AAF28309.1; -  
 DR HSSP: P1140; IABR.  
 DR InterPro: IPR000772; Ricin\_B\_lectin.  
 DR InterPro: IPR001574; RIP.  
 DR Pfam: PF00652; Ricin\_B\_lectin; 6.  
 DR Pfam: PF00161; RIP; 1.  
 DR PRINTS: PRO0396; SHIGARICIN.  
 DR SMART: SM00458; RICIN\_2.  
 DR PROSITE: PS00231; RICIN\_B\_LCTIN; 2.  
 DR PROSITE: PS00275; SHIGA\_RICIN; UNKNOWN\_1.  
 KW Hydrolase; Toxin.  
 SQ SEQUENCE 547 AA; 61248 MW; 355A32C2354A1BD CRC64;

Query Match 8.4%; Score 83; DB 10; Length 547;  
 Best Local Similarity 22.3%; Pred. No. 1.7;  
 Matches 25; Conservative 18; Mismatches 55; Indels 14; Gaps 3;

QY 1 MREPRLEDESSLSLFLQVAVFLAMVGTHTYSHMPSCPSKQDPSSELRSTYVPV 60  
 DB 412 MRQGMRTGNDTS--PFTVSIAGFEKLCMEAHGNSMMLDVC-----DITKEQOMAVYPDG 464  
 QY 61 PLEPAPRNHPESCRASEDGPL-----NSRAISPMRYELDRDLRLPQPL 105  
 DB 465 SIRVQNTNNCLTCEHKGATYVMGCSNMAWASQRRVFKDGIYINLYDM 516

## RESULT 11

ID Q9VS89 PRELIMINARY; PRT: 1394 AA.  
 AC Q9VS89;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE QG7526 protein (Fragment).  
 GN QG7526.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blake J.R.G., Champ E.M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunlop B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,  
 RA Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matell B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.H.,  
 RA Palczolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Sieden-Kiamos I., Stapleton M., Strong R., Sun E.,  
 RA Spletter E., Spreading A.C., Stappleton M., Ventner E., Wang X.,  
 RA Svitskas R., Tector C., Turner R., Ventner E., Weissbach J.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Skupski M.P., Smith T.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AEO03558; AAF50538.1; -.  
 DR HSSP: P00736; IAPQ.  
 DR Flybase: FBgn0035798; CG7526.  
 DR InterPro: IPR000152; Asx\_hydroxyl.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR001881; EGF Ca.  
 DR InterPro: IPR003410; Hyalin.  
 DR InterPro: IPR000436; Sush1-SCR\_CCP.  
 DR InterPro: IPR001491; Thrombomodulin.  
 DR Pfam: PF00008; EGF\_11.  
 DR Pfam: PF00084; sush1\_2.  
 DR PRINTS: PR00907; THROMBOMODULN.  
 DR SMART: SM00032; CCP\_2.  
 DR SMART: SM00179; EGF\_CA\_9.  
 DR SMART: SM00001; ASX\_HYDROXYL; 8.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 8.  
 DR PROSITE: PS01186; EGF\_2; 9.  
 DR PROSITE: PS01187; EGF\_CA; 10.  
 DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.  
 KW NON\_TER 1394 1394  
 FT SEQUENCE 1394 AA: 152269 MW: CD29380E3162F68A CRC64;  
 SQ

Query Match 8.2%; Score 81; DB 5; Length 1394;  
 Best Local Similarity 26.5%; Pred. No. 7.8;  
 Matches 27; Conservative 8; Mismatches 41; Indels 26; Gaps 5;

OY 72 ESCRASEDGPLNSRAISPRVYELDLNLPDLYHARCLCPHCVSLQTSHPDGRNSE 131  
 DB 322 DCDTLENNOLN-----RTKCAHECDLPREGSY--RCVCKRGYLSLSDQH----- 364  
 OY 132 LLYHNGTVFYRRPCHGKGTNR---GYCLERLRYSLACVC 170  
 DB 365 -----SCLVQESPCSTREKGVCKSPCTCLASE-DNTSFSFCIC 400

RESULT 12  
 O9NKZ8 PRELIMINARY: PRT: 379 AA.  
 AC O9NKZ8;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DT

DE HgtrpN3 protein (Fragment).  
 GN HgtrpN3.  
 OS Eptatretus burgeri (Inshore hagfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotretuli; Myxiniiformes;  
 CC Eukaryota; Metazoa; Chordata; Craniata; Hyperotretuli; Myxiniiformes;  
 OX NCBI\_TaxID=7764;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20219325; PubMed-10754074;  
 RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;  
 RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray;  
 RT divergence of tissue-specific isoform genes in the early evolution of  
 RT vertebrates";  
 RT J. Mol. Evol. 50:302-311(2000).  
 RL EMBL: AB033579; BAA95186.1; -.  
 DR HSSP: P18031; 2HNO  
 DR InterPro: IPR000340; DS\_phosphatase.  
 DR InterPro: IPR000387; Tyr\_phosphatase.  
 DR InterPro: IPR000242; Tyr\_PP.  
 DR Pfam: PF00102; Y\_phosphatase; 1.  
 DR Pfam: PF00700; PRTYPPHPTASE.  
 DR PRINTS: SM00194; PTPC; 1.  
 DR SMART: SM00012; PTPC\_DSPC; 1.  
 DR PROSITE: PS00383; TYR\_PHOSPHATASE\_1; 1.  
 DR PROSITE: PS00056; TYR\_PHOSPHATASE\_2; 1.  
 DR PROSITE: PS50055; TYR\_PHOSPHATASE\_PTP; 1.  
 DR Hydrolyase.  
 KW NON\_TER 1  
 FT SEQUENCE 1 42672 MW: A2493B3FE3D90174 CRC64;  
 SQ

Query Match 8.2%; Score 80.5; DB 13; Length 379;  
 Best Local Similarity 28.0%; Pred. No. 2.1;  
 Matches 33; Conservative 9; Mismatches 45; Indels 31; Gaps 6;

OY 22 AFLAMVGTHTYTHMPSCCKSG---QNTSEELRW-----STVPVPLEP--- 64  
 DB 166 SFLALIGGMHLS--ADACGEGYLDDEDEKMSPEEMFYFAPEPSPSTPPPPPPPKR 223  
 OY 65 --ARPNRHP-----ESCRASEDGPLNS--RAISPRVYELDLNLPDLYHARC 110  
 DB 224 STERNGGPAKSNVYEDLTQTELPNNROYELSPRFEKLDGRCVDEAFGERG 281

RESULT 13  
 O9P914 PRELIMINARY: PRT: 358 AA.  
 AC O9P914;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Nitrate reductase subunit 2 (EC 1.7.99.4).  
 GN NARH.  
 OS Haloarcula marismortui (Halo bacterium marismortui), and  
 OS Haloarcula marismortui subsp. marismortui.  
 OC Archaea; Euryarchaeota; Halo bacteriota; Halobacteriales;  
 CC Halobacteriaceae; Haloarcula.  
 OX NCBI\_TaxID=2238, 122093;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-H.marismortui;  
 RA Yoshimatsu K., Iwasaki T., Fujiwara T.;  
 RT "Sequence and Electron Paramagnetic Resonance Analyses of the Archaea  
 RT Nitrate Reductase NARH from the Denitrifying Halophilic Euryarchaeote  
 RT Haloarcula marismortui";  
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RL (12)  
 RN SEQUENCE FROM N.A.  
 RC SPECIES-H.marismortui subsp. marismortui;  
 RA Yoshimatsu K., Yamamoto A., Fujiwara T.;  
 RT "Sequence analysis of the dissimilatory nitrate reductase from a  
 RT denitrifying halophilic archaeon, Haloarcula marismortui";  
 RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ429077; CAD22070.1; -.

